

Page 11, line 31, after "(rat GRR3)" insert --(SEQ ID NO: 42)--.

Page 12, line 1, after "sequence" insert --(SEQ ID NO: 43)--.

Page 12, line 25, after "consensus sequence" insert --(SEQ ID NO: 44)--.

Page 98, line 18, after "Figure 26" insert --(SEQ ID NO: 44)--.

Page 98, line 30, after "Figure 26" insert --(SEQ ID NO: 44)--.

REMARKS

As described above, the specification has been amended so that the figures are more clearly referenced by the appropriate sequence identification numbers. The amendments are fully supported by the specification, and no new matter has been added.

Respectfully submitted,



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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Fox, Gary M
Jing, Shuqian
Wen, Duanzhi
- (ii) TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTORS
- (iii) NUMBER OF SEQUENCES: 44
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: AMGEN INC
(B) STREET: One Amgen Center Drive
(C) CITY: Thousand Oaks
(D) STATE: CA
(E) COUNTRY: US
(F) ZIP: 91320-1789
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/866,354
(B) FILING DATE: 30-MAY-1997
(C) CLASSIFICATION:
- a (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/837,199
(B) FILING DATE: 14-APR-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/015,907
(B) FILING DATE: 22-APR-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/017,221
(B) FILING DATE: 09-MAY-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Curry, Daniel R.
(B) REGISTRATION NUMBER: 32,727
(C) REFERENCE/DOCKET NUMBER: A-401B

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2568 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 540..1934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | |
|---|---|-----------------|------------|------------|------------|-----|
| AATCTGGCCT | CGGAACACGC | CATTCTCCGC | GCCGCTTCCA | ATAACCACTA | ACATCCCTAA | 60 |
| CGAGCATCCG | AGCCGAGGGC | TCTGCTCGGA | AATCGTCCTG | GCCCAACTCG | GCCCTTCGAG | 120 |
| CTCTCGAAGA | TTACCGCATC | TATTTTTTTT | TTCTTTTTTT | TCTTTTCCTA | GCGCAGATAA | 180 |
| AGTGAGCCCG | GAAAGGGAAG | GAGGGGGCGG | GGACACCATT | GCCCTGAAAG | AATAAATAAG | 240 |
| TAAATAAACA | AACTGGCTCC | TCGCCGCAGC | TGGACGCGGT | CGGTTGAGTC | CAGGTTGGGT | 300 |
| CGGACCTGAA | CCCCTAAAAG | CGGAACCGCC | TCCCGCCCTC | GCCATCCCGG | AGCTGAGTCG | 360 |
| CCGGCGGCGG | TGGCTGCTGC | CAGACCCGGA | GTTTCCTCTT | TCACTGGATG | GAGCTGAACT | 420 |
| TTGGGCGGCC | AGAGCAGCAC | AGCTGTCCGG | GGATCGCTGC | ACGCTGAGCT | CCCTCGGCAA | 480 |
| GACCCAGCGG | CGGCTCGGGA | TTTTTTTGGG | GGGGCGGGGA | CCAGCCCCGC | GCCGGCACC | 539 |
| ATG TTC CTG GCG ACC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC | Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu | 1 5 10 15 | 587 | | | |
| CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC | Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala | 20 25 30 | 635 | | | |
| AGT GAT CAG TGC CTG AAG GAG CAG AGC TGC AGC ACC AAG TAC CGC ACG | Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr | 35 40 45 | 683 | | | |
| CTA AGG CAG TGC GTG GCG GGC AAG GAG ACC AAC TTC AGC CTG GCA TCC | Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser | 50 55 60 | 731 | | | |
| GGC CTG GAG GCC AAG GAT GAG TGC CGC AGC GCC ATG GAG GCC CTG AAG | Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys | 65 70 75 80 | 779 | | | |
| CAG AAG TCG CTC TAC AAC TGC CGC TGC AAG CGG GGT ATG AAG AAG GAG | Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu | 85 90 95 | 827 | | | |
| AAG AAC TGC CTG CGC ATT TAC TGG AGC ATG TAC CAG AGC CTG CAG GGA | Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly | 100 105 110 | 875 | | | |
| AAT GAT CTG CTG GAG GAT TCC CCA TAT GAA CCA GTT AAC AGC AGA TTG | Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu | 115 120 125 | 923 | | | |
| TCA GAT ATA TTC CGG GTG GTC CCA TTC ATA TCA GAT GTT TTT CAG CAA | Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln | 130 135 140 | 971 | | | |
| GTG GAG CAC ATT CCC AAA GGG AAC AAC TGC CTG GAT GCA GCG AAG GCC | Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala | 145 150 155 160 | 1019 | | | |
| TGC AAC CTC GAC GAC ATT TGC AAG AAG TAC AGG TCG GCG TAC ATC ACC | Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr | | 1067 | | | |

| 165 | | | | | | | | 170 | | | | | | | | 175 | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| CCG | TGC | ACC | ACC | AGC | GTG | TCC | AAC | GAT | GTC | TGC | AAC | CGC | CGC | AAG | TGC | 1115 | |
| Pro | Cys | Thr | Thr | Ser | Val | Ser | Asn | Asp | Val | Cys | Asn | Arg | Arg | Lys | Cys | | |
| 180 | | | | | | | | 185 | | | | 190 | | | | | |
| CAC | AAG | GCC | CTC | CGG | CAG | TTC | TTT | GAC | AAG | GTC | CCG | GCC | AAG | CAC | AGC | 1163 | |
| His | Lys | Ala | Leu | Arg | Gln | Phe | Phe | Asp | Lys | Val | Pro | Ala | Lys | His | Ser | | |
| 195 | | | | | | | | 200 | | | | 205 | | | | | |
| TAC | GGA | ATG | CTC | TTC | TGC | TCC | TGC | CGG | GAC | ATC | GCC | TGC | ACA | GAG | CGG | 1211 | |
| Tyr | Gly | Met | Leu | Phe | Cys | Ser | Cys | Arg | Asp | Ile | Ala | Cys | Thr | Glu | Arg | | |
| 210 | | | | | | | | 215 | | | | 220 | | | | | |
| AGG | CGA | CAG | ACC | ATC | GTG | CCT | GTG | TGC | TCC | TAT | GAA | GAG | AGG | GAG | AAG | 1259 | |
| Arg | Arg | Gln | Thr | Ile | Val | Pro | Val | Cys | Ser | Tyr | Glu | Glu | Arg | Glu | Lys | | |
| 225 | | | | | | | | 230 | | | | 235 | | | | 240 | |
| CCC | AAC | TGT | TTG | AAT | TTG | CAG | GAC | TCC | TGC | AAG | ACG | AAT | TAC | ATC | TGC | 1307 | |
| Pro | Asn | Cys | Leu | Asn | Leu | Gln | Asp | Ser | Cys | Lys | Thr | Asn | Tyr | Ile | Cys | | |
| | | | | 245 | | | | | | | | 250 | | | | 255 | |
| AGA | TCT | CGC | CTT | GCG | GAT | TTT | TTT | ACC | AAC | TGC | CAG | CCA | GAG | TCA | AGG | 1355 | |
| Arg | Ser | Arg | Leu | Ala | Asp | Phe | Phe | Thr | Asn | Cys | Gln | Pro | Glu | Ser | Arg | | |
| | | | | 260 | | | | 265 | | | | | | | | 270 | |
| TCT | GTC | AGC | AGC | TGT | CTA | AAG | GAA | AAC | TAC | GCT | GAC | TGC | CTC | CTC | GCC | 1403 | |
| Ser | Val | Ser | Ser | Cys | Leu | Lys | Glu | Asn | Tyr | Ala | Asp | Cys | Leu | Leu | Ala | | |
| | | | | 275 | | | | 280 | | | | 285 | | | | | |
| TAC | TCG | GGG | CTT | ATT | GGC | ACA | GTC | ATG | ACC | CCC | AAC | TAC | ATA | GAC | TCC | 1451 | |
| Tyr | Ser | Gly | Leu | Ile | Gly | Thr | Val | Met | Thr | Pro | Asn | Tyr | Ile | Asp | Ser | | |
| | | | | 290 | | | | 295 | | | | 300 | | | | | |
| AGT | AGC | CTC | AGT | GTG | GCC | CCA | TGG | TGT | GAC | TGC | AGC | AAC | AGT | GGG | AAC | 1499 | |
| Ser | Ser | Leu | Ser | Val | Ala | Pro | Trp | Cys | Asp | Cys | Ser | Asn | Ser | Gly | Asn | | |
| 305 | | | | 310 | | | | | | | | 315 | | | | 320 | |
| GAC | CTA | GAA | GAG | TGC | TTG | AAA | TTT | TTG | AAT | TTC | TTC | AAG | GAC | AAT | ACA | 1547 | |
| Asp | Leu | Glu | Glu | Cys | Leu | Lys | Phe | Leu | Asn | Phe | Phe | Lys | Asp | Asn | Thr | | |
| | | | | 325 | | | | | | | | 330 | | | | 335 | |
| TGT | CTT | AAA | AAT | GCA | ATT | CAA | GCC | TTT | GGC | AAT | GGC | TCC | GAT | GTG | ACC | 1595 | |
| Cys | Leu | Lys | Asn | Ala | Ile | Gln | Ala | Phe | Gly | Asn | Gly | Ser | Asp | Val | Thr | | |
| | | | | 340 | | | | 345 | | | | | | | | 350 | |
| GTG | TGG | CAG | CCA | GCC | TTC | CCA | GTA | CAG | ACC | ACC | ACT | GCC | ACT | ACC | ACC | 1643 | |
| Val | Trp | Gln | Pro | Ala | Phe | Pro | Val | Gln | Thr | Thr | Thr | Ala | Thr | Thr | Thr | | |
| | | | | 355 | | | | 360 | | | | 365 | | | | | |
| ACT | GCC | CTC | CGG | GTT | AAG | AAC | AAG | CCC | CTG | GGG | CCA | GCA | GGG | TCT | GAG | 1691 | |
| Thr | Ala | Leu | Arg | Val | Lys | Asn | Lys | Pro | Leu | Gly | Pro | Ala | Gly | Ser | Glu | | |
| | | | | 370 | | | | 375 | | | | 380 | | | | 385 | |
| AAT | GAA | ATT | CCC | ACT | CAT | GTT | TTG | CCA | CCG | TGT | GCA | AAT | TTA | CAG | GCA | 1739 | |
| Asn | Glu | Ile | Pro | Thr | His | Val | Leu | Pro | Pro | Cys | Ala | Asn | Leu | Gln | Ala | | |
| 385 | | | | 390 | | | | | | | | 395 | | | | 400 | |
| CAG | AAG | CTG | AAA | TCC | AAT | GTG | TCG | GGC | AAT | ACA | CAC | CTC | TGT | ATT | TCC | 1787 | |
| Gln | Lys | Leu | Lys | Ser | Asn | Val | Ser | Gly | Asn | Thr | His | Leu | Cys | Ile | Ser | | |
| | | | | 405 | | | | | | | | 410 | | | | 415 | |
| AAT | GGT | AAT | TAT | GAA | AAA | GAA | GGT | CTC | GGT | GCT | TCC | AGC | CAC | ATA | ACC | 1835 | |
| Asn | Gly | Asn | Tyr | Glu | Lys | Glu | Gly | Leu | Gly | Ala | Ser | Ser | His | Ile | Thr | | |

| 420 | 425 | 430 | |
|--|-----|-----|------|
| ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG | | | 1883 |
| Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu | | | |
| 435 | 440 | 445 | |
| GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA ACA | | | 1931 |
| Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr | | | |
| 450 | 455 | 460 | |
| TCA TAGCTGCATT AAAAAAATAC AATATGGACA TGTA AAAAAGA CAAAAACCAA | | | 1984 |
| Ser | | | |
| 465 | | | |
| GTTATCTGTT TCCTGTTCTC TTGTATAGCT GAAATTCCAG TTTAGGAGCT CAGTTGAGAA | | | 2044 |
| ACAGTTCCAT TCAACTGGAA CATT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT | | | 2104 |
| TTNGGGGCTT CTGTGAAAAA CCTGATGCAG TGCTCCATCC AAATCAGAA GGCTTTGGGA | | | 2164 |
| TATGCTGTAT TTTAAAGGGA CAGTTTGTA CTTGGGCTGT AAAGCAAAT GGGGCTGTGT | | | 2224 |
| TTTCGATGAT GATGATNATC ATGATNATGA TNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN | | | 2284 |
| NNNNNNNNNN GATTTTAACA GTTTTACTTC TGGCCTTTCC TAGCTAGAGA AGGAGTTAAT | | | 2344 |
| ATTTCTAAGG TAACTCCCAT ATCTCCTTTA ATGACATTGA TTTCTAATGA TATAAATTTT | | | 2404 |
| AGCCTACATT GATGCCAAGC TTTTTTGCCA CAAAGAAGAT TCTTACCAAG AGTGGGCTTT | | | 2464 |
| GTGGAACAG CTGGTACTGA TGTTACCTT TATATATGTA CTAGCATTTT CCACGCTGAT | | | 2524 |
| GTTTATGTAC TGTAACAGT TCTGCACTCT TGTACAAAAG AAAA | | | 2568 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Leu | Ala | Thr | Leu | Tyr | Phe | Ala | Leu | Pro | Leu | Leu | Asp | Leu | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Ser | Ala | Glu | Val | Ser | Gly | Gly | Asp | Arg | Leu | Asp | Cys | Val | Lys | Ala |
| | | 20 | | | | | | 25 | | | | | 30 | | |
| Ser | Asp | Gln | Cys | Leu | Lys | Glu | Gln | Ser | Cys | Ser | Thr | Lys | Tyr | Arg | Thr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Arg | Gln | Cys | Val | Ala | Gly | Lys | Glu | Thr | Asn | Phe | Ser | Leu | Ala | Ser |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Leu | Glu | Ala | Lys | Asp | Glu | Cys | Arg | Ser | Ala | Met | Glu | Ala | Leu | Lys |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Gln | Lys | Ser | Leu | Tyr | Asn | Cys | Arg | Cys | Lys | Arg | Gly | Met | Lys | Lys | Glu |
| | | | 85 | | | | | 90 | | | | | | 95 | |

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
 100 105 110
 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
 115 120 125
 Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
 130 135 140
 Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
 145 150 155 160
 Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
 165 170 175
 Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys
 180 185 190
 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
 195 200 205
 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
 210 215 220
 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
 225 230 235 240
 Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
 245 250 255
 Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
 260 265 270
 Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
 275 280 285
 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
 290 295 300
 Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
 305 310 315 320
 Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
 325 330 335
 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
 340 345 350
 Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
 355 360 365
 Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
 370 375 380
 Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
 385 390 395 400
 Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
 405 410 415
 Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
 420 425 430
 Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu

435 440 445
 Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr
 450 455 460
 Ser
 465

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2138 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 302..1705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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AGCTCGCTCT CCCGGGGCAG TGGTGTGGAT GCACCGGAGT TCGGGCGCTG GGCAAGTTGG      60
GTCGGAAC TG AACCCCTGAA AGCGGGTCCG CCTCCCGCCC TCGCGCCCGC CCGGATCTGA      120
GTCGCTGGCG GCGGTGGGCG GCAGAGCGAC GGGGAGTCTG CTCTCACCTT GGATGGAGCT      180
GAACTTTGAG TGGCCAGAGG AGCGCAGTCG CCCGGGGGATC GCTGCACGCT GAGCTCTCTC      240
CCCAGAGACCG GCGGCGGGCT TTGGATTTTG GGGGGGCGGG GACCAGCTGC GCGGCGGCAC      300
C ATG TTC CTA GCC ACT CTG TAC TTC GCG CTG CCA CTC CTG GAT TTG      346
  Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu
    1           5           10           15

CTG ATG TCC GCC GAG GTG AGT GGT GGA GAC CGT CTG GAC TGT GTG AAA      394
Leu Met Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys
           20           25           30

GCC AGC GAT CAG TGC CTG AAG GAA CAG AGC TGC AGC ACC AAG TAC CGC      442
Ala Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg
           35           40           45

ACA CTA AGG CAG TGC GTG GCG GGC AAG GAA ACC AAC TTC AGC CTG ACA      490
Thr Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Thr
           50           55           60

TCC GGC CTT GAG GCC AAG GAT GAG TGC CGT AGC GCC ATG GAG GCC TTG      538
Ser Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu
           65           70           75

AAG CAG AAG TCT CTG TAC AAC TGC CGC TGC AAG CGG GGC ATG AAG AAA      586
Lys Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys
           80           85           90           95

GAG AAG AAT TGT CTG CGT ATC TAC TGG AGC ATG TAC CAG AGC CTG CAG      634
Glu Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln
           100           105           110
  
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| | | | | | | | | | | | | | | | | |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| GGA Gly | AAT Asn | GAC Asp | CTC Leu 115 | CTG Leu | GAA Glu | GAT Asp | TCC Ser | CCG Pro 120 | TAT Tyr | GAG Glu | CCG Pro | GTT Val | AAC Asn 125 | AGC Ser | AGG Arg | 682 |
| TTG Leu | TCA Ser | GAT Asp 130 | ATA Ile | TTC Phe | CGG Arg | GCA Ala | GTC Val 135 | CCG Pro | TTC Phe | ATA Ile | TCA Ser | GAT Asp 140 | GTT Val | TTC Phe | CAG Gln | 730 |
| CAA Gln | GTG Val 145 | GAA Glu | CAC His | ATT Ile | TCC Ser | AAA Lys 150 | GGG Gly | AAC Asn | AAC Asn | TGC Cys | CTG Leu 155 | GAC Asp | GCA Ala | GCC Ala | AAG Lys | 778 |
| GCC Ala 160 | TGC Cys | AAC Asn | CTG Leu | GAC Asp | GAC Asp 165 | ACC Thr | TGT Cys | AAG Lys | AAG Lys | TAC Tyr 170 | AGG Arg | TCG Ser | GCC Ala | TAC Tyr | ATC Ile 175 | 826 |
| ACC Thr | CCC Pro | TGC Cys | ACC Thr 180 | ACC Thr | AGC Ser | ATG Met | TCC Ser | AAC Asn | GAG Glu 185 | GTC Val | TGC Cys | AAC Asn | CGC Arg | CGT Arg 190 | AAG Lys | 874 |
| TGC Cys | CAC His | AAG Lys | GCC Ala 195 | CTC Leu | AGG Arg | CAG Gln | TTC Phe 200 | TTC Phe | GAC Asp | AAG Lys | GTT Val | CCG Pro | GCC Ala 205 | AAG Lys | CAC His | 922 |
| AGC Ser | TAC Tyr | GGG Gly 210 | ATG Met | CTC Leu | TTC Phe | TGC Cys | TCC Ser 215 | TGC Cys | CGG Arg | GAC Asp | ATC Ile | GCC Ala 220 | TGC Cys | ACC Thr | GAG Glu | 970 |
| CGG Arg | CGG Arg 225 | CGA Arg | CAG Gln | ACT Thr | ATC Ile | GTC Val 230 | CCC Pro | GTG Val | TGC Cys | TCC Ser | TAT Tyr 235 | GAA Glu | GAA Glu | CGA Arg | GAG Glu | 1018 |
| AGG Arg 240 | CCC Pro | AAC Asn | TGC Cys | CTG Leu | AGT Ser 245 | CTG Leu | CAA Gln | GAC Asp | TCC Ser | TGC Cys 250 | AAG Lys | ACC Thr | AAT Asn | TAC Tyr | ATC Ile 255 | 1066 |
| TGC Cys | AGA Arg | TCT Ser | CGC Arg | CTT Leu 260 | GCA Ala | GAT Asp | TTT Phe | TTT Phe | ACC Thr 265 | AAC Asn | TGC Cys | CAG Gln | CCA Pro | GAG Glu 270 | TCA Ser | 1114 |
| AGG Arg | TCT Ser | GTC Val | AGC Ser 275 | AAC Asn | TGT Cys | CTT Leu | AAG Lys | GAG Glu 280 | AAC Asn | TAC Tyr | GCA Ala | GAC Asp | TGC Cys 285 | CTC Leu | CTG Leu | 1162 |
| GCC Ala | TAC Tyr | TCG Ser 290 | GGA Gly | CTG Leu | ATT Ile | GGC Gly | ACA Thr 295 | GTC Val | ATG Met | ACT Thr | CCC Pro | AAC Asn 300 | TAC Tyr | GTA Val | GAC Asp | 1210 |
| TCC Ser | AGC Ser 305 | AGC Ser | CTC Leu | AGC Ser | GTG Val | GCA Ala 310 | CCA Pro | TGG Trp | TGT Cys | GAC Asp | TGC Cys 315 | AGC Ser | AAC Asn | AGC Ser | GGC Gly | 1258 |
| AAT Asn 320 | GAC Asp | CTG Leu | GAA Glu | GAC Asp | TGC Cys 325 | TTG Leu | AAA Lys | TTT Phe | CTG Leu | AAT Asn 330 | TTT Phe | TTT Phe | AAG Lys | GAC Asp | AAT Asn 335 | 1306 |
| ACT Thr | TGT Cys | CTC Leu | AAA Lys 340 | AAT Asn | GCA Ala | ATT Ile | CAA Gln | GCC Ala | TTT Phe 345 | GGC Gly | AAT Asn | GGC Gly | TCA Ser | GAT Asp 350 | GTG Val | 1354 |
| ACC Thr | ATG Met | TGG Trp | CAG Gln 355 | CCA Pro | GCC Ala | CCT Pro | CCA Pro | GTC Val 360 | CAG Gln | ACC Thr | ACC Thr | ACT Thr | GCC Ala 365 | ACC Thr | ACT Thr | 1402 |

| | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|------|
| ACC | ACT | GCC | TTC | CGG | GTC | AAG | AAC | AAG | CCT | CTG | GGG | CCA | GCA | GGG | TCT | 1450 |
| Thr | Thr | Ala | Phe | Arg | Val | Lys | Asn | Lys | Pro | Leu | Gly | Pro | Ala | Gly | Ser | |
| | | 370 | | | | | 375 | | | | | 380 | | | | |
| GAG | AAT | GAG | ATC | CCC | ACA | CAC | GTT | TTA | CCA | CCC | TGT | GCG | AAT | TTG | CAG | 1498 |
| Glu | Asn | Glu | Ile | Pro | Thr | His | Val | Leu | Pro | Pro | Cys | Ala | Asn | Leu | Gln | |
| | 385 | | | | | 390 | | | | | 395 | | | | | |
| GCT | CAG | AAG | CTG | AAA | TCC | AAT | GTG | TCG | GGT | AGC | ACA | CAC | CTC | TGT | CTT | 1546 |
| Ala | Gln | Lys | Leu | Lys | Ser | Asn | Val | Ser | Gly | Ser | Thr | His | Leu | Cys | Leu | |
| 400 | | | | | 405 | | | | 410 | | | | | | 415 | |
| TCT | GAT | AGT | GAT | TTC | GGA | AAG | GAT | GGT | CTC | GCT | GGT | GCC | TCC | AGC | CAC | 1594 |
| Ser | Asp | Ser | Asp | Phe | Gly | Lys | Asp | Gly | Leu | Ala | Gly | Ala | Ser | Ser | His | |
| | | | | 420 | | | | | 425 | | | | | 430 | | |
| ATA | ACC | ACA | AAA | TCA | ATG | GCT | GCT | CCT | CCC | AGC | TGC | AGT | CTG | AGC | TCA | 1642 |
| Ile | Thr | Thr | Lys | Ser | Met | Ala | Ala | Pro | Pro | Ser | Cys | Ser | Leu | Ser | Ser | |
| | | | 435 | | | | | 440 | | | | | 445 | | | |
| CTG | CCG | GTG | CTG | ATG | CTC | ACC | GCC | CTT | GCT | GCC | CTG | TTA | TCT | GTA | TCG | 1690 |
| Leu | Pro | Val | Leu | Met | Leu | Thr | Ala | Leu | Ala | Ala | Leu | Leu | Ser | Val | Ser | |
| | | 450 | | | | | 455 | | | | | 460 | | | | |
| TTG | GCA | GAA | ACG | TCG | TAGCTGCATC | CGGGAAAACA | GTATGAAAAG | ACAAAAGAGA | | | | | | | | 1745 |
| Leu | Ala | Glu | Thr | Ser | | | | | | | | | | | | |
| | 465 | | | | | | | | | | | | | | | |
| ACCAAGTATT | CTGTCCCTGT | CCTCTTGTAT | ATCTGAAAAT | CCAGTTTTAA | AAGCTCCGTT | | | | | | | | | | | 1805 |
| GAGAAGCAGT | TTCACCCAAC | TGGAACTCTT | TCCTTGTTTT | TAAGAAAGCT | TGTGGCCCTC | | | | | | | | | | | 1865 |
| AGGGGCTTCT | GTTGAAGAAC | TGCTACAGGG | CTAATTCCAA | ACCCATAAGG | CTCTGGGGCG | | | | | | | | | | | 1925 |
| TGGTGCGGCT | TAAGGGGACC | ATTTGCACCA | TGTAAAGCAA | GCTGGGCTTA | TCATGTGTTT | | | | | | | | | | | 1985 |
| GATGGTGAGG | ATGGTAGTGG | TGATGATGAT | GGTAATTTTA | ACAGCTTGAA | CCCTGTTCTC | | | | | | | | | | | 2045 |
| TCTACTGGTT | AGGAACAGGA | GATACTATTG | ATAAAGATTC | TTCCATGTCT | TACTCAGCAG | | | | | | | | | | | 2105 |
| CATTGCCTTC | TGAAGACAGG | CCCGCAGCCG | TCG | | | | | | | | | | | | | 2138 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Phe | Leu | Ala | Thr | Leu | Tyr | Phe | Ala | Leu | Pro | Leu | Leu | Asp | Leu | Leu | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Met | Ser | Ala | Glu | Val | Ser | Gly | Gly | Asp | Arg | Leu | Asp | Cys | Val | Lys | Ala | |
| | | 20 | | | | | | 25 | | | | | 30 | | | |
| Ser | Asp | Gln | Cys | Leu | Lys | Glu | Gln | Ser | Cys | Ser | Thr | Lys | Tyr | Arg | Thr | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Leu | Arg | Gln | Cys | Val | Ala | Gly | Lys | Glu | Thr | Asn | Phe | Ser | Leu | Thr | Ser | |

| 50 | | | | | 55 | | | | | 60 | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Gly 65 | Leu | Glu | Ala | Lys | Asp 70 | Glu | Cys | Arg | Ser | Ala 75 | Met | Glu | Ala | Leu | Lys 80 |
| Gln | Lys | Ser | Leu | Tyr 85 | Asn | Cys | Arg | Cys | Lys 90 | Arg | Gly | Met | Lys | Lys 95 | Glu |
| Lys | Asn | Cys | Leu 100 | Arg | Ile | Tyr | Trp | Ser 105 | Met | Tyr | Gln | Ser | Leu 110 | Gln | Gly |
| Asn | Asp | Leu 115 | Leu | Glu | Asp | Ser | Pro 120 | Tyr | Glu | Pro | Val | Asn 125 | Ser | Arg | Leu |
| Ser | Asp 130 | Ile | Phe | Arg | Ala | Val 135 | Pro | Phe | Ile | Ser | Asp 140 | Val | Phe | Gln | Gln |
| Val 145 | Glu | His | Ile | Ser | Lys 150 | Gly | Asn | Asn | Cys | Leu 155 | Asp | Ala | Ala | Lys | Ala 160 |
| Cys | Asn | Leu | Asp | Asp 165 | Thr | Cys | Lys | Lys | Tyr 170 | Arg | Ser | Ala | Tyr | Ile 175 | Thr |
| Pro | Cys | Thr | Thr 180 | Ser | Met | Ser | Asn | Glu 185 | Val | Cys | Asn | Arg | Arg 190 | Lys | Cys |
| His | Lys | Ala 195 | Leu | Arg | Gln | Phe | Phe 200 | Asp | Lys | Val | Pro | Ala 205 | Lys | His | Ser |
| Tyr | Gly 210 | Met | Leu | Phe | Cys | Ser 215 | Cys | Arg | Asp | Ile | Ala 220 | Cys | Thr | Glu | Arg |
| Arg 225 | Arg | Gln | Thr | Ile | Val 230 | Pro | Val | Cys | Ser | Tyr 235 | Glu | Glu | Arg | Glu | Arg 240 |
| Pro | Asn | Cys | Leu | Ser 245 | Leu | Gln | Asp | Ser | Cys 250 | Lys | Thr | Asn | Tyr | Ile 255 | Cys |
| Arg | Ser | Arg | Leu 260 | Ala | Asp | Phe | Phe 265 | Thr | Asn | Cys | Gln | Pro | Glu 270 | Ser | Arg |
| Ser | Val | Ser 275 | Asn | Cys | Leu | Lys | Glu 280 | Asn | Tyr | Ala | Asp | Cys 285 | Leu | Leu | Ala |
| Tyr | Ser 290 | Gly | Leu | Ile | Gly | Thr 295 | Val | Met | Thr | Pro | Asn 300 | Tyr | Val | Asp | Ser |
| Ser 305 | Ser | Leu | Ser | Val | Ala 310 | Pro | Trp | Cys | Asp | Cys 315 | Ser | Asn | Ser | Gly | Asn 320 |
| Asp | Leu | Glu | Asp | Cys 325 | Leu | Lys | Phe | Leu | Asn 330 | Phe | Phe | Lys | Asp | Asn 335 | Thr |
| Cys | Leu | Lys | Asn 340 | Ala | Ile | Gln | Ala | Phe 345 | Gly | Asn | Gly | Ser | Asp 350 | Val | Thr |
| Met | Trp | Gln 355 | Pro | Ala | Pro | Pro | Val 360 | Gln | Thr | Thr | Thr | Ala 365 | Thr | Thr | Thr |
| Thr | Ala 370 | Phe | Arg | Val | Lys | Asn 375 | Lys | Pro | Leu | Gly | Pro 380 | Ala | Gly | Ser | Glu |
| Asn 385 | Glu | Ile | Pro | Thr | His 390 | Val | Leu | Pro | Pro | Cys 395 | Ala | Asn | Leu | Gln | Ala 400 |

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "1 to 539 is -237 to 301 of
Figure 5 Gdnfr"

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 540..1937

| | | | | | | |
|---|------------|------------|------------|------------|-------------|-----|
| AATCTGGCCT | CGGAACACGC | CATTCTCCGC | GCCGCTTCCA | ATAACCACTA | ACATCCCCTAA | 60 |
| CGAGCATCCG | AGCCGAGGGC | TCTGCTCGGA | AATCGTCCTG | GCCCAACTCG | GCCCTTTCGAG | 120 |
| CTCTCGAAGA | TTACCGCATC | TATTTTTTTT | TTCTTTTTTT | TCTTTTCCTA | GCGCAGATAA | 180 |
| AGTGAGCCCG | GAAAGGGAAG | GAGGGGGCGG | GGACACCATT | GCCCTGAAAG | AATAAATAAG | 240 |
| TAAATAAACA | AACTGGCTCC | TCGCCGCAGC | TGGACGCGGT | CGGTTGAGTC | CAGGTTGGGT | 300 |
| CGGACCTGAA | CCCCTAAAAG | CGGAACCGCC | TCCCGCCCTC | GCCATCCCGG | AGCTGAGTCG | 360 |
| CCGGCGGCGG | TGGCTGCTGC | CAGACCCGGA | GTTTCCTCTT | TCACTGGATG | GAGCTGAACT | 420 |
| TTGGGCGGCC | AGAGCAGCAC | AGCTGTCCGG | GGATCGCTGC | ACGCTGAGCT | CCCTCGGCAA | 480 |
| GACCCAGCGG | CGGCTCGGGA | TTTTTTTGGG | GGGGCGGGGA | CCAGCCCCGC | GCCGGCACC | 539 |
| ATG TTC CTG GCG ACC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC | 587 | | | | | |
| Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu | | | | | | |
| 1 5 10 15 | | | | | | |
| CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC | 635 | | | | | |
| Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala | | | | | | |

| 20 | | | | 25 | | | | 30 | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| AGT | GAT | CAG | TGC | CTG | AAG | GAG | CAG | AGC | TGC | AGC | ACC | AAG | TAC | CGC | ACG | 683 |
| Ser | Asp | Gln | Cys | Leu | Lys | Glu | Gln | Ser | Cys | Ser | Thr | Lys | Tyr | Arg | Thr | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| CTA | AGG | CAG | TGC | GTG | GCG | GGC | AAG | GAG | ACC | AAC | TTC | AGC | CTG | GCA | TCC | 731 |
| Leu | Arg | Gln | Cys | Val | Ala | Gly | Lys | Glu | Thr | Asn | Phe | Ser | Leu | Ala | Ser | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| GGC | CTG | GAG | GCC | AAG | GAT | GAG | TGC | CGC | AGC | GCC | ATG | GAG | GCC | CTG | AAG | 779 |
| Gly | Leu | Glu | Ala | Lys | Asp | Glu | Cys | Arg | Ser | Ala | Met | Glu | Ala | Leu | Lys | |
| 65 | | | | 70 | | | | | | 75 | | | | | 80 | |
| CAG | AAG | TCG | CTC | TAC | AAC | TGC | CGC | TGC | AAG | CGG | GGT | ATG | AAG | AAG | GAG | 827 |
| Gln | Lys | Ser | Leu | Tyr | Asn | Cys | Arg | Cys | Lys | Arg | Gly | Met | Lys | Lys | Glu | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| AAG | AAC | TGC | CTG | CGC | ATT | TAC | TGG | AGC | ATG | TAC | CAG | AGC | CTG | CAG | GGA | 875 |
| Lys | Asn | Cys | Leu | Arg | Ile | Tyr | Trp | Ser | Met | Tyr | Gln | Ser | Leu | Gln | Gly | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| AAT | GAT | CTG | CTG | GAG | GAT | TCC | CCA | TAT | GAA | CCA | GTT | AAC | AGC | AGA | TTG | 923 |
| Asn | Asp | Leu | Leu | Glu | Asp | Ser | Pro | Tyr | Glu | Pro | Val | Asn | Ser | Arg | Leu | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| TCA | GAT | ATA | TTC | CGG | GTG | GTC | CCA | TTC | ATA | TCA | GAT | GTT | TTT | CAG | CAA | 971 |
| Ser | Asp | Ile | Phe | Arg | Val | Val | Pro | Phe | Ile | Ser | Asp | Val | Phe | Gln | Gln | |
| | 130 | | | | 135 | | | | | | 140 | | | | | |
| GTG | GAG | CAC | ATT | CCC | AAA | GGG | AAC | AAC | TGC | CTG | GAT | GCA | GCG | AAG | GCC | 1019 |
| Val | Glu | His | Ile | Pro | Lys | Gly | Asn | Asn | Cys | Leu | Asp | Ala | Ala | Lys | Ala | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| TGC | AAC | CTC | GAC | GAC | ATT | TGC | AAG | AAG | TAC | AGG | TCG | GCG | TAC | ATC | ACC | 1067 |
| Cys | Asn | Leu | Asp | Asp | Ile | Cys | Lys | Lys | Tyr | Arg | Ser | Ala | Tyr | Ile | Thr | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| CCG | TGC | ACC | ACC | AGC | GTG | TCC | AAN | GAT | GTC | TGC | AAC | CGC | CGC | AAG | TGC | 1115 |
| Pro | Cys | Thr | Thr | Ser | Val | Ser | Xaa | Asp | Val | Cys | Asn | Arg | Arg | Lys | Cys | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| CAC | AAG | GCC | CTC | CGG | CAG | TTC | TTT | GAC | AAG | GTC | CCG | GCC | AAG | CAC | AGC | 1163 |
| His | Lys | Ala | Leu | Arg | Gln | Phe | Phe | Asp | Lys | Val | Pro | Ala | Lys | His | Ser | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| TAC | GGA | ATG | CTC | TTC | TGC | TCC | TGC | CGG | GAC | ATC | GCC | TGC | ACA | GAG | CGG | 1211 |
| Tyr | Gly | Met | Leu | Phe | Cys | Ser | Cys | Arg | Asp | Ile | Ala | Cys | Thr | Glu | Arg | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| AGG | CGA | CAG | ACC | ATC | GTG | CCT | GTG | TGC | TCC | TAT | GAA | GAG | AGG | GAG | AAG | 1259 |
| Arg | Arg | Gln | Thr | Ile | Val | Pro | Val | Cys | Ser | Tyr | Glu | Glu | Arg | Glu | Lys | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| CCC | AAC | TGT | TTG | AAT | TTG | CAG | GAC | TCC | TGC | AAG | ACG | AAT | TAC | ATC | TGC | 1307 |
| Pro | Asn | Cys | Leu | Asn | Leu | Gln | Asp | Ser | Cys | Lys | Thr | Asn | Tyr | Ile | Cys | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| AGA | TCT | CGC | CTT | GCG | GAT | TTT | TTT | ACC | AAC | TGC | CAG | CCA | GAG | TCA | AGG | 1355 |
| Arg | Ser | Arg | Leu | Ala | Asp | Phe | Phe | Thr | Asn | Cys | Gln | Pro | Glu | Ser | Arg | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| TCT | GTC | AGC | AGC | TGT | CTA | AAG | GAA | AAC | TAC | GCT | GAC | TGC | CTC | CTC | GCC | 1403 |
| Ser | Val | Ser | Ser | Cys | Leu | Lys | Glu | Asn | Tyr | Ala | Asp | Cys | Leu | Leu | Ala | |

TCTAAGGTAA CTCCCATATC TCCTTTAATG ACATTGATTT CTAATGATAT AAATTTTCAGC 2407

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CTACATTGAT GCCAAGCTTT TTTGCCACAA AGAAGATTCT TACCAAGAGT GGGCTTTGTG      2467
GAAACAGCTG GTACTGATGT TCACCTTTAT ATATGTACTA GCATTTTCCA CGCTGATGTT      2527
TATGTACTGT AAACAGTTCT GCACTCTTGT AAAAAAGAAA AAACACCTGT CACATCCAAA      2587
TATAGTATCT GTCTTTTCGT CAAAATAGAG AGTGGGGAAT GAGTGTGCCG ATTCAATACC      2647
TCAATCCCTG AACGACACTC TCCTAATCCT AAGCCTTACC TGAGTGAGAA GCCCTTTACC      2707
TAACAAAAGT CCAATATAGC TGAAATGTCG CTCTAATACT CTTTACACAT ATGAGGTTAT      2767
ATGTAGAAAA AAATTTTACT ACTAAATGAT TTCAACTATT GGCTTTCTAT ATTTTGAAAG      2827
TAATGATATT GTCTCATTTT TTTACTGATG GTTTAATACA AAATACACAG AGCTTGTTTC      2887
CCCTCATAAG TAGTGTTTCG TCTGATATGA ACTTCACAAA TACAGCTCAT CAAAAGCAGA      2947
CTCTGAGAAG CCTCGTGCTG TAGCAGAAAG TTCTGCATCA TGTGACTGTG GACAGGCAGG      3007
AGGAAACAGA ACAGACAAGC ATTGCTCTTTT GTCATTGCTC GAAGTGCAAG CGTGCATACC      3067
TGTGGAGGGA ACTGGTGGCT GCTTGTAAT GTTCTGCAGC ATCTCTTGAC ACACCTGTCA      3127
TGACACAATC CAGTACCTTG GTTTTCAGGT TATCTGACAA AGGCAGCTTT GATTGGGACA      3187
TGGAGGCATG GGCAGGCCGG AA                                          3209

```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
 1           5           10
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
 20           25           30
Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
 35           40           45
Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
 50           55           60
Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
 65           70           75
Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
 85           90           95
Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
100          105          110
Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
115          120          125

```

[illegible]

465

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..508
- (D) OTHER INFORMATION: /note= "1 to 508 is -237 to 272 of Figure 5 Hsgr-21af"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

TCTGGCCTCG GAACACGCCA TTCTCCGCGC CGCTTCCAAT AACCACTAAC ATCCCTAACG      60
AGCATCCGAG CCGAGGGGCTC TGCTCGGAAA TCGTCCTGGC CCAACTCGGC CCTTCGAGCT      120
CTCGAAGATT ACCGCATCTA TTTTTTTTTT CTTTTTTTTT TTTTCCTAGC GCAGATAAAG      180
TGAGCCCGGA AAGGGAAGGA GGGGGCGGGG ACACCATTCG CCTGAAAGAA TAAATAAGTA      240
AATAAACAAA CTGGCTCCTC GCCGCAGCTG GACGCGGTCG GTTGAGTCCA GGTGGGGTCG      300
GACCTGAACC CCTAAAAGCG GAACCGCCTC CCGCCCTCGC CATCCCGGAG CTGAGTCGCC      360
GGCGGCGGTG GCTGCTGCCA GACCCGGAGT TTCCTCTTTC ACTGGATGGA GCTGAACTTT      420
GGGCGGCCAG AGCAGCACAG CTGTCCGGGG ATCGCTGCAC GCTGAGCTCC CTCGGCAAGA      480
CCCAGCGGCG GCTCGGGATT TTTTGGGG                                     508

```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..510
- (D) OTHER INFORMATION: /note= "1 to 510 is -237 to 272 of Figure 5 Hsgr-21bf"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA ACATCCCTAA      60
CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG GCCCAACTCG GCCCTTCGAG      120

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CTCTCGAAGA TTACCGCATC TATTTTTTTTTT TTCTTTTTTTT TCTTTTCCTA GCGCAGATAA      180
AGTGAGCCCG GAAAGGGAAG GAGGGGGCGG GGACACCATT GCCCTGAAAG AATAAATAAG      240
TAAATAAACA AACTGGCTCC TCGCCGCAGC TGGACGCGGT CGGTTGAGTC CAGGTTGGGT      300
CGGACCTGAA CCCCTAAAAG CGGAACCGCC TCCC GCCCTC GCCATCCCGG AGCTGAGTCG      360
CCGGCGGCGG TGGCTGCTGC CAGACCCGGA GTTTCCTCTT TCACTGGATG GAGCTGAACT      420
TTGGGCGGCC AGAGCAGCAC AGCTGTCCGG GGATCGCTGC ACGCTGAGCT CCCTCGGCAA      480
GACCCAGCGG CGGCTCGGGA TTTTTTTGGG      510

```

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1927 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 538..1926

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..537

(D) OTHER INFORMATION: /note= "1 to 537 is -235 to 301 of Figure 5 21acon"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

TCTGGCCTCG GAACACGCCA TTCTCCGCGC CGCTTCCAAT AACCACTAAC ATCCCTAACG      60
AGCATCCGAG CCGAGGGCTC TGCTCGGAAA TCGTCCTGGC CCAACTCGGC CCTTCGAGCT      120
CTCGAAGATT ACCGCATCTA TTTTTTTTTT CTTTTTTTTT TTTTCCTAGC GCAGATAAAG      180
TGAGCCCGGA AAGGGAAGGA GGGGGCGGGG ACACCATTGC CCTGAAAGAA TAAATAAGTA      240
AATAAACAAA CTGGCTCCTC GCCGCAGCTG GACGCGGTGC GTTGAGTCCA GGTTGGGTGC      300
GACCTGAACC CCTAAAAGCG GAACCGCCTC CCGCCCTCGC CATCCCGGAG CTGAGTCGCC      360
GGCGGCGGTG GCTGCTGCCA GACCCGGAGT TTCTCTTTT ACTGGATGGA GCTGAACTTT      420
GGGCGGCCAG AGCAGCACAG CTGTCCGGGG ATCGCTGCAC GCTGAGCTCC CTCGGCAAGA      480
CCCAGCGGCG GCTCGGGATT TTTTTGGGGG GGCGGGGACC AGCCCCGCGC CGGCACC      537
ATG TTC CTG GCG NCC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC      585
Met Phe Leu Ala Xaa Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
  1           5           10           15

CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC      633
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
          20           25           30

```

| | | | | | | | | | | | | | | | | |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| AGT Ser | GAT Asp | CAG Gln 35 | TGC Cys | CTG Leu | AAG Lys | GAG Glu | CAG Gln 40 | AGC Ser | TGC Cys | AGC Ser | ACC Thr | AAG Lys 45 | TAC Tyr | CGC Arg | ACG Thr | 681 |
| CTA Leu | AGG Arg 50 | CAG Gln | TGC Cys | GTG Val | GCG Ala | GGC Gly 55 | AAG Lys | GAG Glu | ACC Thr | AAC Asn | TTC Phe 60 | AGC Ser | CTG Leu | GCA Ala | TCC Ser | 729 |
| GGC Gly 65 | CTG Leu | GAG Glu | GCC Ala | AAG Lys | GAT Asp 70 | GAG Glu | TGC Cys | CGC Arg | AGC Ser | GCC Ala 75 | ATG Met | GAG Glu | GCC Ala | CTG Leu | AAG Lys 80 | 777 |
| CAG Gln | AAG Lys | TCG Ser | CTC Leu | TAC Tyr 85 | AAC Asn | TGC Cys | CGC Arg | TGC Cys | AAG Lys 90 | CGG Arg | GGT Gly | ATG Met | AAG Lys 95 | AAG Lys | GAG Glu | 825 |
| AAG Lys | AAC Asn | TGC Cys | CTG Leu 100 | CGC Arg | ATT Ile | TAC Tyr | TGG Trp | AGC Ser 105 | ATG Met | TAC Tyr | CAG Gln | AGC Ser | CTG Leu 110 | CAG Gln | GGA Gly | 873 |
| AAT Asn | GAT Asp 115 | CTG Leu | CTG Leu | GAG Glu | GAT Asp | TCC Ser | CCA Pro 120 | TAT Tyr | GAA Glu | CCA Pro | GTT Val | AAC Asn 125 | AGC Ser | AGA Arg | TTG Leu | 921 |
| TCA Ser 130 | GAT Asp | ATA Ile | TTC Phe | CGG Arg | GTG Val | GTC Val 135 | CCA Pro | TTC Phe | ATA Ile | TCA Ser | GAT Asp 140 | GTT Val | TTT Phe | CAG Gln | CAA Gln | 969 |
| GTG Val 145 | GAG Glu | CAC His | ATT Ile | CCC Pro | AAA Lys 150 | GGG Gly | AAC Asn | AAC Asn | TGC Cys | CTG Leu 155 | GAT Asp | GCA Ala | GCG Ala | AAG Lys | GCC Ala 160 | 1017 |
| TGC Cys | AAC Asn | CTC Leu | GAC Asp | GAC Asp 165 | ATT Ile | TGC Cys | AAG Lys | AAG Lys | TAC Tyr 170 | AGG Arg | TCG Ser | GCG Ala | TAC Tyr | ATC Ile 175 | ACC Thr | 1065 |
| CCG Pro | TGC Cys | ACC Thr 180 | ACC Thr | AGC Ser | GTG Val | TCC Ser | AAC Asn | GAT Asp 185 | GTC Val | TGC Cys | AAC Asn | CGC Arg | CGC Arg | AAG Lys | TGC Cys | 1113 |
| CAC His | AAG Lys 195 | GCC Ala | CTC Leu | CGG Arg | CAG Gln | TTC Phe | TTT Phe 200 | GAC Asp | AAG Lys | GTC Val | CCG Pro | GCC Ala 205 | AAG Lys | CAC His | AGC Ser | 1161 |
| TAC Tyr 210 | GGA Gly | ATG Met | CTC Leu | TTC Phe | TGC Cys | TCC Ser 215 | TGC Cys | CGG Arg | GAC Asp | ATC Ile | GCC Ala 220 | TGC Cys | ACA Thr | GAG Glu | CGG Arg | 1209 |
| AGG Arg 225 | CGA Arg | CAG Gln | ACC Thr | ATC Ile | GTG Val 230 | CCT Pro | GTG Val | TGC Cys | TCC Ser | TAT Tyr 235 | GAA Glu | GAG Glu | AGG Arg | GAG Glu | AAG Lys 240 | 1257 |
| CCC Pro | AAC Asn | TGT Cys | TTG Leu | AAT Asn 245 | TTG Leu | CAG Gln | GAC Asp | TCC Ser | TGC Cys 250 | AAG Lys | ACG Thr | AAT Asn | TAC Tyr | ATC Ile 255 | TGC Cys | 1305 |
| AGA Arg | TCT Ser | CGC Arg | CTT Leu 260 | GCG Ala | GAT Asp | TTT Phe | TTT Phe 265 | ACC Thr | AAC Asn | TGC Cys | CAG Gln | CCA Pro | GAG Glu 270 | TCA Ser | AGG Arg | 1353 |
| TCT Ser | GTC Val | AGC Ser 275 | AGC Ser | TGT Cys | CTA Leu | AAG Lys | GAA Glu 280 | AAC Asn | TAC Tyr | GCT Ala | GAC Asp | TGC Cys 285 | CTC Leu | CTC Leu | GCC Ala | 1401 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| TAC | TCG | GGG | CTT | ATT | GGC | ACA | GTC | ATG | ACC | CCC | AAC | TAC | ATA | GAC | TCC | 1449 |
| Tyr | Ser | Gly | Leu | Ile | Gly | Thr | Val | Met | Thr | Pro | Asn | Tyr | Ile | Asp | Ser | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| AGT | AGC | CTC | AGT | GTG | GCC | CCA | TGG | TGT | GAC | TGC | AGC | AAC | AGT | GGG | AAC | 1497 |
| Ser | Ser | Leu | Ser | Val | Ala | Pro | Trp | Cys | Asp | Cys | Ser | Asn | Ser | Gly | Asn | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| GAC | CTA | GAA | GAG | TGC | TTG | AAA | TTT | TTG | AAT | TTC | TTC | AAG | GAC | AAT | ACA | 1545 |
| Asp | Leu | Glu | Glu | Cys | Leu | Lys | Phe | Leu | Asn | Phe | Phe | Lys | Asp | Asn | Thr | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| TGT | CTT | AAA | AAT | GCA | ATT | CAA | GCC | TTT | GGC | AAT | GGC | TCC | GAT | GTG | ACC | 1593 |
| Cys | Leu | Lys | Asn | Ala | Ile | Gln | Ala | Phe | Gly | Asn | Gly | Ser | Asp | Val | Thr | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| GTG | TGG | CAG | CCA | GCC | TTC | CCA | GTA | CAG | ACC | ACC | ACT | GCC | ACT | ACC | ACC | 1641 |
| Val | Trp | Gln | Pro | Ala | Phe | Pro | Val | Gln | Thr | Thr | Thr | Ala | Thr | Thr | Thr | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| ACT | GCC | CTC | CGG | GTT | AAG | AAC | AAG | CCC | CTG | GGG | CCA | GCA | GGG | TCT | GAG | 1689 |
| Thr | Ala | Leu | Arg | Val | Lys | Asn | Lys | Pro | Leu | Gly | Pro | Ala | Gly | Ser | Glu | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| AAT | GAA | ATT | CCC | ACT | CAT | GTT | TTG | CCA | CCG | TGT | GCA | AAT | TTA | CAG | GCA | 1737 |
| Asn | Glu | Ile | Pro | Thr | His | Val | Leu | Pro | Pro | Cys | Ala | Asn | Leu | Gln | Ala | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| CAG | AAG | CTG | AAA | TCC | AAT | GTG | TCG | GGC | AAT | ACA | CAC | CTC | TGT | ATT | TCC | 1785 |
| Gln | Lys | Leu | Lys | Ser | Asn | Val | Ser | Gly | Asn | Thr | His | Leu | Cys | Ile | Ser | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| AAT | GGT | AAT | TAT | GAA | AAA | GAA | GGT | CTC | GGT | GCT | TCC | AGC | CAC | ATA | ACC | 1833 |
| Asn | Gly | Asn | Tyr | Glu | Lys | Glu | Gly | Leu | Gly | Ala | Ser | Ser | His | Ile | Thr | |
| | | | 420 | | | | 425 | | | | | | 430 | | | |
| ACA | AAA | TCA | ATG | GCT | GCT | CCT | CCA | AGC | TGT | GGT | CTG | AGC | CCA | CTG | CTG | 1881 |
| Thr | Lys | Ser | Met | Ala | Ala | Pro | Pro | Ser | Cys | Gly | Leu | Ser | Pro | Leu | Leu | |
| | | 435 | | | | | 440 | | | | | 445 | | | | |
| GTC | CTG | GTG | GTA | ACC | GCT | CTG | TCC | ACC | CTA | TTA | TCT | TTA | ACA | GAA | | 1926 |
| Val | Leu | Val | Val | Thr | Ala | Leu | Ser | Thr | Leu | Leu | Ser | Leu | Thr | Glu | | |
| | 450 | | | | | 455 | | | | | 460 | | | | | |
| A | | | | | | | | | | | | | | | | 1927 |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Phe | Leu | Ala | Xaa | Leu | Tyr | Phe | Ala | Leu | Pro | Leu | Leu | Asp | Leu | Leu | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Leu | Ser | Ala | Glu | Val | Ser | Gly | Gly | Asp | Arg | Leu | Asp | Cys | Val | Lys | Ala | |
| | | 20 | | | | | | 25 | | | | | 30 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Asp | Gln | Cys | Leu | Lys | Glu | Gln | Ser | Cys | Ser | Thr | Lys | Tyr | Arg | Thr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Arg | Gln | Cys | Val | Ala | Gly | Lys | Glu | Thr | Asn | Phe | Ser | Leu | Ala | Ser |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Leu | Glu | Ala | Lys | Asp | Glu | Cys | Arg | Ser | Ala | Met | Glu | Ala | Leu | Lys |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Gln | Lys | Ser | Leu | Tyr | Asn | Cys | Arg | Cys | Lys | Arg | Gly | Met | Lys | Lys | Glu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Lys | Asn | Cys | Leu | Arg | Ile | Tyr | Trp | Ser | Met | Tyr | Gln | Ser | Leu | Gln | Gly |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Asn | Asp | Leu | Leu | Glu | Asp | Ser | Pro | Tyr | Glu | Pro | Val | Asn | Ser | Arg | Leu |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ser | Asp | Ile | Phe | Arg | Val | Val | Pro | Phe | Ile | Ser | Asp | Val | Phe | Gln | Gln |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Val | Glu | His | Ile | Pro | Lys | Gly | Asn | Asn | Cys | Leu | Asp | Ala | Ala | Lys | Ala |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Cys | Asn | Leu | Asp | Asp | Ile | Cys | Lys | Lys | Tyr | Arg | Ser | Ala | Tyr | Ile | Thr |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Pro | Cys | Thr | Thr | Ser | Val | Ser | Asn | Asp | Val | Cys | Asn | Arg | Arg | Lys | Cys |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| His | Lys | Ala | Leu | Arg | Gln | Phe | Phe | Asp | Lys | Val | Pro | Ala | Lys | His | Ser |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Tyr | Gly | Met | Leu | Phe | Cys | Ser | Cys | Arg | Asp | Ile | Ala | Cys | Thr | Glu | Arg |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Arg | Arg | Gln | Thr | Ile | Val | Pro | Val | Cys | Ser | Tyr | Glu | Glu | Arg | Glu | Lys |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Pro | Asn | Cys | Leu | Asn | Leu | Gln | Asp | Ser | Cys | Lys | Thr | Asn | Tyr | Ile | Cys |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Arg | Ser | Arg | Leu | Ala | Asp | Phe | Phe | Thr | Asn | Cys | Gln | Pro | Glu | Ser | Arg |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ser | Val | Ser | Ser | Cys | Leu | Lys | Glu | Asn | Tyr | Ala | Asp | Cys | Leu | Leu | Ala |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Tyr | Ser | Gly | Leu | Ile | Gly | Thr | Val | Met | Thr | Pro | Asn | Tyr | Ile | Asp | Ser |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Ser | Ser | Leu | Ser | Val | Ala | Pro | Trp | Cys | Asp | Cys | Ser | Asn | Ser | Gly | Asn |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Asp | Leu | Glu | Glu | Cys | Leu | Lys | Phe | Leu | Asn | Phe | Phe | Lys | Asp | Asn | Thr |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Cys | Leu | Lys | Asn | Ala | Ile | Gln | Ala | Phe | Gly | Asn | Gly | Ser | Asp | Val | Thr |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Val | Trp | Gln | Pro | Ala | Phe | Pro | Val | Gln | Thr | Thr | Thr | Ala | Thr | Thr | Thr |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Thr | Ala | Leu | Arg | Val | Lys | Asn | Lys | Pro | Leu | Gly | Pro | Ala | Gly | Ser | Glu |

| | | | | |
|---|-----|-----|-----|-----|
| 370 | | 375 | | 380 |
| Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala | | | | |
| 385 | | 390 | | 395 |
| Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser | | | | |
| | 405 | | 410 | 415 |
| Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr | | | | |
| | 420 | | 425 | 430 |
| Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu | | | | |
| | 435 | | 440 | 445 |
| Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu | | | | |
| 450 | | 455 | | 460 |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1929 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 540..1928

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..539

(D) OTHER INFORMATION: /note= "1 to 539 is -237 to 301 of Figure 5 21bcon"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | | | | | | |
|---|------------|------------|------------|------------|------------|-----|
| AATCTGGCCT | CGGAACACGC | CATTCTCCGC | GCCGCTTCCA | ATAACCACTA | ACATCCCTAA | 60 |
| CGAGCATCCG | AGCCGAGGGC | TCTGCTCGGA | AATCGTCCTG | GCCCAACTCG | GCCCTTCGAG | 120 |
| CTCTCGAAGA | TTACCGCATC | TATTTTTTTT | TTCTTTTTTT | TCTTTTCCTA | GCGCAGATAA | 180 |
| AGTGAGCCCG | GAAAGGGAAG | GAGGGGGCGG | GGACACCATT | GCCCTGAAAG | AATAAATAAG | 240 |
| TAAATAAACA | AACTGGCTCC | TCGCCGCAGC | TGGACGCGGT | CGGTTGAGTC | CAGGTTGGGT | 300 |
| CGGACCTGAA | CCCCTAAAAG | CGGAACCGCC | TCCCGCCCTC | GCCATCCCGG | AGCTGAGTCG | 360 |
| CCGGCGGCGG | TGGCTGCTGC | CAGACCCGGA | GTTTCCTCTT | TCACTGGATG | GAGCTGAACT | 420 |
| TTGGGCGGCC | AGAGCAGCAC | AGCTGTCCGG | GGATCGCTGC | ACGCTGAGCT | CCCTCGGCAA | 480 |
| GACCCAGCGG | CGGCTCGGGA | TTTTTTTGGG | GGGGCGGGGA | CCAGCCCCGC | GCCGGCACC | 539 |
| ATG TTC CTG GCG ACC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC | | | | | | 587 |
| Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu | | | | | | |
| 1 | 5 | | 10 | | 15 | |
| CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC | | | | | | 635 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Leu | Ser | Ala | Glu | Val | Ser | Gly | Gly | Asp | Arg | Leu | Asp | Cys | Val | Lys | Ala | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| AGT | GAT | CAG | TGC | CTG | AAG | GAG | CAG | AGC | TGC | AGC | ACC | AAG | TAC | CGC | ACG | 683 |
| Ser | Asp | Gln | Cys | Leu | Lys | Glu | Gln | Ser | Cys | Ser | Thr | Lys | Tyr | Arg | Thr | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| CTA | AGG | CAG | TGC | GTG | GCG | GGC | AAG | GAG | ACC | AAC | TTC | AGC | CTG | GCA | TCC | 731 |
| Leu | Arg | Gln | Cys | Val | Ala | Gly | Lys | Glu | Thr | Asn | Phe | Ser | Leu | Ala | Ser | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| GGC | CTG | GAG | GCC | AAG | GAT | GAG | TGC | CGC | AGC | GCC | ATG | GAG | GCC | CTG | AAG | 779 |
| Gly | Leu | Glu | Ala | Lys | Asp | Glu | Cys | Arg | Ser | Ala | Met | Glu | Ala | Leu | Lys | |
| 65 | | | | 70 | | | | | | 75 | | | | | 80 | |
| CAG | AAG | TCG | CTC | TAC | AAC | TGC | CGC | TGC | AAG | CGG | GGT | ATG | AAG | AAG | GAG | 827 |
| Gln | Lys | Ser | Leu | Tyr | Asn | Cys | Arg | Cys | Lys | Arg | Gly | Met | Lys | Lys | Glu | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| AAG | AAC | TGC | CTG | CGC | ATT | TAC | TGG | AGC | ATG | TAC | CAG | AGC | CTG | CAG | GGA | 875 |
| Lys | Asn | Cys | Leu | Arg | Ile | Tyr | Trp | Ser | Met | Tyr | Gln | Ser | Leu | Gln | Gly | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| AAT | GAT | CTG | CTG | GAG | GAT | TCC | CCA | TAT | GAA | CCA | GTT | AAC | AGC | AGA | TTG | 923 |
| Asn | Asp | Leu | Leu | Glu | Asp | Ser | Pro | Tyr | Glu | Pro | Val | Asn | Ser | Arg | Leu | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| TCA | GAT | ATA | TTC | CGG | GTG | GTC | CCA | TTC | ATA | TCA | GAT | GTT | TTT | CAG | CAA | 971 |
| Ser | Asp | Ile | Phe | Arg | Val | Val | Pro | Phe | Ile | Ser | Asp | Val | Phe | Gln | Gln | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| GTG | GAG | CAC | ATT | CCC | AAA | GGG | AAC | AAC | TGC | CTG | GAT | GCA | GCG | AAG | GCC | 1019 |
| Val | Glu | His | Ile | Pro | Lys | Gly | Asn | Asn | Cys | Leu | Asp | Ala | Ala | Lys | Ala | |
| 145 | | | | 150 | | | | | 155 | | | | | | 160 | |
| TGC | AAC | CTC | GAC | GAC | ATT | TGC | AAG | AAG | TAC | AGG | TCG | GCG | TAC | ATC | ACC | 1067 |
| Cys | Asn | Leu | Asp | Asp | Ile | Cys | Lys | Lys | Tyr | Arg | Ser | Ala | Tyr | Ile | Thr | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| CCG | TGC | ACC | ACC | AGC | GTG | TCC | AAC | GAT | GTC | TGC | AAC | CGC | CGC | AAG | TGC | 1115 |
| Pro | Cys | Thr | Thr | Ser | Val | Ser | Asn | Asp | Val | Cys | Asn | Arg | Arg | Lys | Cys | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| CAC | AAG | GCC | CTC | CGG | CAG | TTC | TTT | GAC | AAG | GTC | CCG | GCC | AAG | CAC | AGC | 1163 |
| His | Lys | Ala | Leu | Arg | Gln | Phe | Phe | Asp | Lys | Val | Pro | Ala | Lys | His | Ser | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| TAC | GGA | ATG | CTC | TTC | TGC | TCC | TGC | CGG | GAC | ATC | GCC | TGC | ACA | GAG | CGG | 1211 |
| Tyr | Gly | Met | Leu | Phe | Cys | Ser | Cys | Arg | Asp | Ile | Ala | Cys | Thr | Glu | Arg | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| AGG | CGA | CAG | ACC | ATC | GTG | CCT | GTG | TGC | TCC | TAT | GAA | GAG | AGG | GAG | AAG | 1259 |
| Arg | Arg | Gln | Thr | Ile | Val | Pro | Val | Cys | Ser | Tyr | Glu | Glu | Arg | Glu | Lys | |
| 225 | | | | 230 | | | | | | 235 | | | | | 240 | |
| CCC | AAC | TGT | TTG | AAT | TTG | CAG | GAC | TCC | TGC | AAG | ACG | AAT | TAC | ATC | TGC | 1307 |
| Pro | Asn | Cys | Leu | Asn | Leu | Gln | Asp | Ser | Cys | Lys | Thr | Asn | Tyr | Ile | Cys | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| AGA | TCT | CGC | CTT | GCG | GAT | TTT | TTT | ACC | AAC | TGC | CAG | CCA | GAG | TCA | AGG | 1355 |
| Arg | Ser | Arg | Leu | Ala | Asp | Phe | Phe | Thr | Asn | Cys | Gln | Pro | Glu | Ser | Arg | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| TCT | GTC | AGC | AGC | TGT | CTA | AAG | GAA | AAC | TAC | GCT | GAC | TGC | CTC | CTC | GCC | 1403 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Ser | Val | Ser | Ser | Cys | Leu | Lys | Glu | Asn | Tyr | Ala | Asp | Cys | Leu | Leu | Ala | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| TAC | TCG | GGG | CTT | ATT | GGC | ACA | GTC | ATG | ACC | CCC | AAC | TAC | ATA | GAC | TCC | 1451 |
| Tyr | Ser | Gly | Leu | Ile | Gly | Thr | Val | Met | Thr | Pro | Asn | Tyr | Ile | Asp | Ser | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| AGT | AGC | CTC | AGT | GTG | GCC | CCA | TGG | TGT | GAC | TGC | AGC | AAC | AGT | GGG | AAC | 1499 |
| Ser | Ser | Leu | Ser | Val | Ala | Pro | Trp | Cys | Asp | Cys | Ser | Asn | Ser | Gly | Asn | |
| 305 | | | | | 310 | | | | | 315 | | | | 320 | | |
| GAC | CTA | GAA | GAG | TGC | TTG | AAA | TTT | TTG | AAT | TTC | TTC | AAG | GAC | AAT | ACA | 1547 |
| Asp | Leu | Glu | Glu | Cys | Leu | Lys | Phe | Leu | Asn | Phe | Phe | Lys | Asp | Asn | Thr | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| TGT | CTT | AAA | AAT | GCA | ATT | CAA | GCC | TTT | GGC | AAT | GGC | TCC | GAT | GTG | ACC | 1595 |
| Cys | Leu | Lys | Asn | Ala | Ile | Gln | Ala | Phe | Gly | Asn | Gly | Ser | Asp | Val | Thr | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| GTG | TGG | CAG | CCA | GCC | TTC | CCA | GTA | CAG | ACC | ACC | ACT | GCC | ACT | ACC | ACC | 1643 |
| Val | Trp | Gln | Pro | Ala | Phe | Pro | Val | Gln | Thr | Thr | Thr | Ala | Thr | Thr | Thr | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| ACT | GCC | CTC | CGG | GTT | AAG | AAC | AAG | CCC | CTG | GGG | CCA | GCA | GGG | TCT | GAG | 1691 |
| Thr | Ala | Leu | Arg | Val | Lys | Asn | Lys | Pro | Leu | Gly | Pro | Ala | Gly | Ser | Glu | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| AAT | GAA | ATT | CCC | ACT | CAT | GTT | TTG | CCA | CCG | TGT | GCA | AAT | TTA | CAG | GCA | 1739 |
| Asn | Glu | Ile | Pro | Thr | His | Val | Leu | Pro | Pro | Cys | Ala | Asn | Leu | Gln | Ala | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| CAG | AAG | CTG | AAA | TCC | AAT | GTG | TCG | GGC | AAT | ACA | CAC | CTC | TGT | ATT | TCC | 1787 |
| Gln | Lys | Leu | Lys | Ser | Asn | Val | Ser | Gly | Asn | Thr | His | Leu | Cys | Ile | Ser | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| AAT | GGT | AAT | TAT | GAA | AAA | GAA | GGT | CTC | GGT | GCT | TCC | AGC | CAC | ATA | ACC | 1835 |
| Asn | Gly | Asn | Tyr | Glu | Lys | Glu | Gly | Leu | Gly | Ala | Ser | Ser | His | Ile | Thr | |
| | | | 420 | | | | 425 | | | | | | 430 | | | |
| ACA | AAA | TCA | ATG | GCT | GCT | CCT | CCA | AGC | TGT | GGT | CTG | AGC | CCA | CTG | CTG | 1883 |
| Thr | Lys | Ser | Met | Ala | Ala | Pro | Pro | Ser | Cys | Gly | Leu | Ser | Pro | Leu | Leu | |
| | | 435 | | | | | 440 | | | | | 445 | | | | |
| GTC | CTG | GTG | GTA | ACC | GCT | CTG | TCC | ACC | CTA | TTA | TCT | TTA | ACA | GAA | | 1928 |
| Val | Leu | Val | Val | Thr | Ala | Leu | Ser | Thr | Leu | Leu | Ser | Leu | Thr | Glu | | |
| | 450 | | | | | 455 | | | | | 460 | | | | | |
| A | | | | | | | | | | | | | | | | 1929 |

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 463 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Phe | Leu | Ala | Thr | Leu | Tyr | Phe | Ala | Leu | Pro | Leu | Leu | Asp | Leu | Leu | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| M | V | L | A | T | L | Y | F | A | L | P | L | L | N | L | L | |

Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
 20 25 30
 Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
 35 40 45
 Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
 50 55 60
 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
 65 70 75 80
 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
 85 90 95
 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
 100 105 110
 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
 115 120 125
 Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
 130 135 140
 Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
 145 150 155 160
 Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
 165 170 175
 Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys
 180 185 190
 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
 195 200 205
 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
 210 215 220
 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
 225 230 235 240
 Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
 245 250 255
 Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
 260 265 270
 Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
 275 280 285
 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
 290 295 300
 Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
 305 310 315 320
 Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
 325 330 335
 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
 340 345 350
 Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr

| | | |
|---|-----|-----|
| 355 | 360 | 365 |
| Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu | | |
| 370 | 375 | 380 |
| Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala | | |
| 385 | 390 | 395 |
| Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser | | |
| | 405 | 410 |
| Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr | | |
| | 420 | 425 |
| Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu | | |
| | 435 | 440 |
| Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu | | |
| | 450 | 455 |
| | | 460 |

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..699
- (D) OTHER INFORMATION: /note= "1 to 699 is 814 to 1512 of

Figure 5 Hsgr-29a"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | |
|---|-----|
| G TCG GCG TAC ATC ACC CCG TGC ACC ACC AGC GTG TCC AAT GAT GTC | 46 |
| Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val | |
| 1 5 10 15 | |
| TGC AAC CGC CGC AAG TGC CAC AAG GCC CTC CGG CAG TTC TTT GAC AAG | 94 |
| Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys | |
| 20 25 30 | |
| GTC CCG GCC AAG CAC AGC TAC GGA ATG CTC TTC TGC TCC TGC CGG GAC | 142 |
| Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp | |
| 35 40 45 | |
| ATC GCC TGC ACA GAG CGG AGG CGA CAG ACC ATC GTG CCT GTG TGC TCC | 190 |
| Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser | |
| 50 55 60 | |
| TAT GAA GAG AGG GAG AAG CCC AAC TGT TTG AAT TTG CAG GAC TCC TGC | 238 |
| Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys | |
| 65 70 75 | |

| | | | | | | | | | | | | | | | | |
|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| AAG Lys 80 | ACG Thr | AAT Asn | TAC Tyr | ATC Ile | TGC Cys 85 | AGA Arg | TCT Ser | CGC Arg | CTT Leu | GCG Ala 90 | GAT Asp | TTT Phe | TTT Phe | ACC Thr | AAC Asn 95 | 286 |
| TGC Cys | CAG Gln | CCA Pro | GAG Glu | TCA Ser 100 | AGG Arg | TCT Ser | GTC Val | AGC Ser 105 | AGC Cys | TGT Leu | CTA Lys | AAG Glu | GAA Asn 110 | AAC Tyr | TAC | 334 |
| GCT Ala | GAC Asp | TGC Cys | CTC Leu 115 | CTC Leu | GCC Ala | TAC Tyr | TCG Ser | GGG Gly 120 | CTT Leu | ATT Ile | GGC Gly | ACA Thr | GTC Val 125 | ATG Met | ACC Thr | 382 |
| CCC Pro | AAC Asn | TAC Tyr 130 | ATA Ile | GAC Asp | TCC Ser | AGT Ser | AGC Ser 135 | CTC Leu | AGT Ser | GTG Val | GCC Ala 140 | CCA Pro | TGG Trp | TGT Cys | GAC Asp | 430 |
| TGC Cys 145 | AGC Ser | AAC Asn | AGT Ser | GGG Gly | AAC Asn | GAC Asp 150 | CTA Leu | GAA Glu | GAG Glu | TGC Cys 155 | TTG Leu | AAA Lys | TTT Phe | TTG Leu | AAT Asn | 478 |
| TTC Phe 160 | TTC Phe | AAG Lys | GAC Asp | AAT Asn | ACA Thr 165 | TGT Cys | CTT Leu | AAA Lys | AAT Asn | GCA Ala 170 | ATT Ile | CAA Gln | GCC Ala | TTT Phe | GGC Gly 175 | 526 |
| AAT Asn | GGC Gly | TCC Ser | GAT Asp | GTG Val 180 | ACC Thr | GTG Val | TGG Trp | CAG Gln | CCA Pro 185 | GCC Ala | TTC Phe | CCA Pro | GTA Val | CAG Gln 190 | ACC Thr | 574 |
| ACC Thr | ACT Thr | GCC Ala | GCT Ala 195 | ACC Thr | ACC Thr | ACT Thr | GCC Ala | CTC Leu 200 | CGG Arg | GTT Val | AAG Lys | AAC Asn | AAG Lys 205 | CCC Pro | CTG Leu | 622 |
| GGG Gly | CCA Pro | GCA Ala 210 | GGG Gly | TCT Ser | GAG Glu | AAT Asn | GAA Glu 215 | ATT Ile | CCC Pro | ACT Thr | CAT His | GTT Val 220 | TTG Leu | CCA Pro | CCG Pro | 670 |
| TGT Cys 225 | GCA Ala | AAT Asn | TTA Leu | CAG Gln | GCA Ala | CAG Gln | AAG Lys 230 | CTG Leu | AA | | | | | | | 699 |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

| | | | | | | | | | | | | | | | |
|----------|-----------|-----------|-----------|----------|-----|-----------|-----------|-----------|-----|-----|-----------|-----------|-----------|-----------|-----|
| Ser 1 | Ala | Tyr | Ile | Thr 5 | Pro | Cys | Thr | Thr 10 | Ser | Val | Ser | Asn | Asp | Val 15 | Cys |
| Asn | Arg | Arg | Lys 20 | Cys | His | Lys | Ala | Leu 25 | Arg | Gln | Phe | Phe | Asp 30 | Lys | Val |
| Pro | Ala | Lys 35 | His | Ser | Tyr | Gly | Met 40 | Leu | Phe | Cys | Ser | Cys 45 | Arg | Asp | Ile |
| Ala | Cys 50 | Thr | Glu | Arg | Arg | Arg 55 | Gln | Thr | Ile | Val | Pro 60 | Val | Cys | Ser | Tyr |

Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys
 65 70 75 80
 Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys
 85 90 95
 Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala
 100 105 110
 Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro
 115 120 125
 Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys
 130 135 140
 Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe
 145 150 155 160
 Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn
 165 170 175
 Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr
 180 185 190
 Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly
 195 200 205
 Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys
 210 215 220
 Ala Asn Leu Gln Ala Gln Lys Leu
 225 230

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..886

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..2157

(D) OTHER INFORMATION: /note= "1 to 2157 is 814 to 2971 of Figure 5 29brc"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| G | TCG | GCG | TAC | ATC | ACC | CCG | TGC | ACC | ACC | AGC | GTG | TCC | AAT | GAT | GTC | 46 |
| Ser | Ala | Tyr | Ile | Thr | Pro | Cys | Thr | Thr | Ser | Val | Ser | Asn | Asp | Val | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| TGC | AAC | CGC | CGC | AAG | TGC | CAC | AAG | GCC | CTC | CGG | CAG | TTC | TTT | GAC | AAG | 94 |
| Cys | Asn | Arg | Arg | Lys | Cys | His | Lys | Ala | Leu | Arg | Gln | Phe | Phe | Asp | Lys | |
| | | | | 20 | | | | | 25 | | | | | 30 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTC | CCG | GCC | AAG | CAC | AGC | TAC | GGA | ATG | CTC | TTC | TGC | TCC | TGC | CGG | GAC | 142 |
| Val | Pro | Ala | Lys | His | Ser | Tyr | Gly | Met | Leu | Phe | Cys | Ser | Cys | Arg | Asp | |
| | | | 35 | | | | | 40 | | | | | 45 | | | |
| ATC | GCC | TGC | ACA | GAG | CGG | AGG | CGA | CAG | ACC | ATC | GTG | CCT | GTG | TGC | TCC | 190 |
| Ile | Ala | Cys | Thr | Glu | Arg | Arg | Arg | Gln | Thr | Ile | Val | Pro | Val | Cys | Ser | |
| | | 50 | | | | | 55 | | | | | 60 | | | | |
| TAT | GAA | GAG | AGG | GAG | AAG | CCC | AAC | TGT | TTG | AAT | TTG | CAG | GAC | TCC | TGC | 238 |
| Tyr | Glu | Glu | Arg | Glu | Lys | Pro | Asn | Cys | Leu | Asn | Leu | Gln | Asp | Ser | Cys | |
| | 65 | | | | | 70 | | | | | 75 | | | | | |
| AAG | ACG | AAT | TAC | ATC | TGC | AGA | TCT | CGC | CTT | GCG | GAT | TTT | TTT | ACC | AAC | 286 |
| Lys | Thr | Asn | Tyr | Ile | Cys | Arg | Ser | Arg | Leu | Ala | Asp | Phe | Phe | Thr | Asn | |
| 80 | | | | | 85 | | | | | 90 | | | | | 95 | |
| TGC | CAG | CCA | GAG | TCA | AGG | TCT | GTC | AGC | AGC | TGT | CTA | AAG | GAA | AAC | TAC | 334 |
| Cys | Gln | Pro | Glu | Ser | Arg | Ser | Val | Ser | Ser | Cys | Leu | Lys | Glu | Asn | Tyr | |
| | | | | 100 | | | | 105 | | | | | | 110 | | |
| GCT | GAC | TGC | CTC | CTC | GCC | TAC | TCG | GGG | CTT | ATT | GGC | ACA | GTC | ATG | ACC | 382 |
| Ala | Asp | Cys | Leu | Leu | Ala | Tyr | Ser | Gly | Leu | Ile | Gly | Thr | Val | Met | Thr | |
| | | | 115 | | | | | 120 | | | | | 125 | | | |
| CCC | AAC | TAC | ATA | GAC | TCC | AGT | AGC | CTC | AGT | GTG | GCC | CCA | TGG | TGT | GAC | 430 |
| Pro | Asn | Tyr | Ile | Asp | Ser | Ser | Ser | Leu | Ser | Val | Ala | Pro | Trp | Cys | Asp | |
| | | 130 | | | | 135 | | | | | | 140 | | | | |
| TGC | AGC | AAC | AGT | GGG | AAC | GAC | CTA | GAA | GAG | TGC | TTG | AAA | TTT | TTG | AAT | 478 |
| Cys | Ser | Asn | Ser | Gly | Asn | Asp | Leu | Glu | Glu | Cys | Leu | Lys | Phe | Leu | Asn | |
| | 145 | | | | | 150 | | | | | 155 | | | | | |
| TTC | TTC | AAG | GAC | AAT | ACA | TGT | CTT | AAA | AAT | GCA | ATT | CAA | GCC | TTT | GGC | 526 |
| Phe | Phe | Lys | Asp | Asn | Thr | Cys | Leu | Lys | Asn | Ala | Ile | Gln | Ala | Phe | Gly | |
| 160 | | | | | 165 | | | | | 170 | | | | | 175 | |
| AAT | GGC | TCC | GAT | GTG | ACC | GTG | TGG | CAG | CCA | GCC | TTC | CCA | GTA | CAG | ACC | 574 |
| Asn | Gly | Ser | Asp | Val | Thr | Val | Trp | Gln | Pro | Ala | Phe | Pro | Val | Gln | Thr | |
| | | | | 180 | | | | 185 | | | | | | 190 | | |
| ACC | ACT | GCC | GCT | ACC | ACC | ACT | GCC | CTC | CGG | GTT | AAG | AAC | AAG | CCC | CTG | 622 |
| Thr | Thr | Ala | Ala | Thr | Thr | Thr | Ala | Leu | Arg | Val | Lys | Asn | Lys | Pro | Leu | |
| | | | 195 | | | | | 200 | | | | | 205 | | | |
| GGG | CCA | GCA | GGG | TCT | GAG | AAT | GAA | ATT | CCC | ACT | CAT | GTT | TTG | CCA | CCG | 670 |
| Gly | Pro | Ala | Gly | Ser | Glu | Asn | Glu | Ile | Pro | Thr | His | Val | Leu | Pro | Pro | |
| | | 210 | | | | | 215 | | | | | 220 | | | | |
| TGT | GCA | AAT | TTA | CAG | GCA | CAG | AAG | CTG | AAA | TCC | AAT | GTG | TCG | GGC | AAT | 718 |
| Cys | Ala | Asn | Leu | Gln | Ala | Gln | Lys | Leu | Lys | Ser | Asn | Val | Ser | Gly | Asn | |
| | 225 | | | | | 230 | | | | | 235 | | | | | |
| ACA | CAC | CTC | TGT | ATT | TCC | AAT | GGT | AAT | TAT | GAA | AAA | GAA | GGT | CTC | GGT | 766 |
| Thr | His | Leu | Cys | Ile | Ser | Asn | Gly | Asn | Tyr | Glu | Lys | Glu | Gly | Leu | Gly | |
| 240 | | | | | 245 | | | | | 250 | | | | | 255 | |
| GCT | TCC | AGC | CAC | ATA | ACC | ACA | AAA | TCA | ATG | GCT | GCT | CCT | CCA | AGC | TGT | 814 |
| Ala | Ser | Ser | His | Ile | Thr | Thr | Lys | Ser | Met | Ala | Ala | Pro | Pro | Ser | Cys | |
| | | | | 260 | | | | | 265 | | | | | 270 | | |
| GGT | CTG | AGC | CCA | CTG | CTG | GTC | CTG | GTG | GTA | ACC | GCT | CTG | TCC | ACC | CTA | 862 |
| Gly | Leu | Ser | Pro | Leu | Leu | Val | Leu | Val | Val | Thr | Ala | Leu | Ser | Thr | Leu | |
| | | | 275 | | | | | 280 | | | | | 285 | | | |

```

TTA TCT TTA ACA GAA ACA TCA TAG CTGCATTAAA AAAATACAAT ATGGACATGT      916
Leu Ser Leu Thr Glu Thr Ser *
      290                      295

AAAAAGACAA AAACCAAGTT ATCTGTTTCC TGTTCCTCTTG TATAGCTGAA ATTCCAGTTT      976
AGGAGCTCAG TTGAGAAACA GTTCCATTCA ACTGGAACAT TTTTTTTTTT CCTTTTAAGA      1036
AAGCTTCTTG TGATCCTTCG GGGCTTCTGT GAAAAACCTG ATGCAGTGCT CCATCCAAAC      1096
TCAGAAGGCT TTGGGATATG CTGTATTTTA AAGGGACAGT TTGTAACCTG GGCTGTAAAG      1156
CAAACCTGGGG CTGTGTTTTTC GATGATGATG ATCATCATGA TCATGATNNN NNNNNNNNNN      1216
NNNNNNNNNN NNNNNNNNNN NNNNNNGATT TTAACAGTTT TACTTCTGGC CTTTCCTAGC      1276
TAGAGAAGGA GTTAATATTT CTAAGGTAAC TCCCATATCT CCTTTAATGA CATTGATTTT      1336
TAATGATATA AATTTTCAGCC TACATTGATG CCAAGCTTTT TTGCCACAAA GAAGATTCTT      1396
ACCAAGAGTG GGCTTTGTGG AAACAGCTGG TACTGATGTT CACCTTTATA TATGTACTAG      1456
CATTTTCCAC GCTGATGTTT ATGTACTGTA AACAGTTCTG CACTCTTGTA CAAAAGAAAA      1516
AACACCTGTC ACATCCAAAT ATAGTATCTG TCTTTTCGTC AAAATAGAGA GTGGGGAATG      1576
AGTGTGCCGA TTCAATACCT CAATCCCTGA ACGACACTCT CCTAATCCTA AGCCTTACCT      1636
GAGTGAGAAG CCCTTTACCT AACAAAAGTC CAATATAGCT GAAATGTCGC TCTAATACTC      1696
TTTACACATA TGAGGTTATA TGTAGAAAAA AATTTTACTA CTAAATGATT TCAACTATTG      1756
GCTTTCTATA TTTTGAAAGT AATGATATTG TCTCATTTTT TTAAGTATGG TTTAATACAA      1816
AATACACAGA GCTTGTTTCC CCTCATAAGT AGTGTTTCGCT CTGATATGAA CTTACAAAAT      1876
ACAGCTCATC AAAAGCAGAC TCTGAGAAGC CTCGTGCTGT AGCAGAAAGT TCTGCATCAT      1936
GTGACTGTGG ACAGGCAGGA GGAAACAGAA CAGACAAGCA TTGTCTTTTG TCATTGCTCG      1996
AAGTGCAAGC GTGCATACCT GTGGAGGGAA CTGGTGCTG CTTGTAAATG TTCTGCAGCA      2056
TCTCTTGACA CACTTGTCAT GACACAATCC AGTACCTTGG TTTTCAGGTT ATCTGACAAA      2116
GGCAGCTTTG ATTGGGACAT GGAGGCATGG GCAGGCCGGA A                        2157

```

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 295 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys
 1           5           10           15

Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val
      20           25           30

```

Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile
 35 40 45
 Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr
 50 55 60
 Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys
 65 70 75 80
 Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys
 85 90 95
 Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala
 100 105 110
 Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro
 115 120 125
 Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys
 130 135 140
 Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe
 145 150 155 160
 Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn
 165 170 175
 Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr
 180 185 190
 Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly
 195 200 205
 Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys
 210 215 220
 Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr
 225 230 235 240
 His Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala
 245 250 255
 Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly
 260 265 270
 Leu Ser Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu
 275 280 285
 Ser Leu Thr Glu Thr Ser *
 290 295

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 659 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..658

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..659
(D) OTHER INFORMATION: /note= "1 to 659 is 1033 to 1691 of
Figure 5 Hsgr-21ar"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

| | |
|---|-----|
| G AAT TTG CAG GAC TCC TGC AAG ACG AAT TAC ATC TGC AGA TCT CGC | 46 |
| Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg | |
| 1 5 10 15 | |
| CTT GCG GAT TTT TTT ACC AAC TGC CAG CCA GAG TCA AGG TCT GTC AGC | 94 |
| Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser | |
| 20 25 30 | |
| AGC TGT CTA AAG GAA AAC TAC GCT GAC TGC CTC CTC GCC TAC TCG GGG | 142 |
| Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly | |
| 35 40 45 | |
| CTT ATT GGC ACA GTC ATG ACC CCC AAC TAC ATA GAC TCC AGT AGC CTC | 190 |
| Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu | |
| 50 55 60 | |
| AGT GTG GCC CCA TGG TGT GAC TGC AGC AAC AGT GGG AAC GAC CTA GAA | 238 |
| Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu | |
| 65 70 75 | |
| GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG GAC AAT ACA TGT CTT AAA | 286 |
| Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys | |
| 80 85 90 95 | |
| AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC GAT GTG ACC GTG TGG CAG | 334 |
| Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln | |
| 100 105 110 | |
| CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC ACT ACC ACC ACT GCC CTC | 382 |
| Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu | |
| 115 120 125 | |
| CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA GGG TCT GAG AAT GAA ATT | 430 |
| Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile | |
| 130 135 140 | |
| CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT TTA CAG GCA CAG AAG CTG | 478 |
| Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu | |
| 145 150 155 | |
| AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC TGT ATT TCC AAT GGT AAT | 526 |
| Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn | |
| 160 165 170 175 | |
| TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC CAC ATA ACC ACA AAA TCA | 574 |
| Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser | |
| 180 185 190 | |
| ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG GTC CTG GTG | 622 |
| Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val | |
| 195 200 205 | |

GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA A
 Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
 210 215

659

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu
 1 5 10 15
 Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser
 20 25 30
 Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu
 35 40 45
 Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser
 50 55 60
 Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu
 65 70 75 80
 Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn
 85 90 95
 Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro
 100 105 110
 Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg
 115 120 125
 Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro
 130 135 140
 Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys
 145 150 155 160
 Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr
 165 170 175
 Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met
 180 185 190
 Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val
 195 200 205
 Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
 210 215

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 630 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..629

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..630

(D) OTHER INFORMATION: /note= "1 to 630 is 1062 to 1691 of Figure 5 Hsgr-21br"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

| | |
|---|-----|
| AC ATC TGC AGA TCT CGC CTT GCG GAT TTT TTT ACC AAC TGC CAG CCA | 47 |
| Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro | |
| 1 5 10 15 | |
| GAG TCA AGG TCT GTC AGC AGC TGT CTA AAG GAA AAC TAC GCT GAC TGC | 95 |
| Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys | |
| 20 25 30 | |
| CTC CTC GCC TAC TCG GGG CTT ATT GGC ACA GTC ATG ACC CCC AAC TAC | 143 |
| Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr | |
| 35 40 45 | |
| ATA GAC TCC AGT AGC CTC AGT GTG GCC CCA TGG TGT GAC TGC AGC AAC | 191 |
| Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn | |
| 50 55 60 | |
| AGT GGG AAC GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG | 239 |
| Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys | |
| 65 70 75 | |
| GAC AAT ACA TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC | 287 |
| Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser | |
| 80 85 90 95 | |
| GAT GTG ACC GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC | 335 |
| Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala | |
| 100 105 110 | |
| ACT ACC ACC ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA | 383 |
| Thr Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala | |
| 115 120 125 | |
| GGG TCT GAG AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT | 431 |
| Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn | |
| 130 135 140 | |
| TTA CAG GCA CAG AAG CTG AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC | 479 |
| Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu | |
| 145 150 155 | |
| TGT ATT TCC AAT GGT AAT TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC | 527 |
| Cys Ile Ser Asn Gly Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser | |
| 160 165 170 175 | |
| CAC ATA ACC ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC | 575 |
| His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser | |

[illegible]

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

[illegible]

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1075 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..445

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..1075

(D) OTHER INFORMATION: /note= "1 to 1075 is 1255 to 2330
of Figure 5 Hsgr-2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

| | |
|---|-----|
| T GGG AAC GAC CTA GAA GAG TGC TTG AAA TTT TTG AAT TTC TTC AAG | 46 |
| Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys | |
| 1 5 10 15 | |
| GAC AAT ACA TGT CTT AAA AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC | 94 |
| Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser | |
| 20 25 30 | |
| GAT GTG ACC GTG TGG CAG CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC | 142 |
| Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala | |
| 35 40 45 | |
| ACT ACC ACC ACT GCC CTC CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA | 190 |
| Thr Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala | |
| 50 55 60 | |
| GGG TCT GAG AAT GAA ATT CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT | 238 |
| Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn | |
| 65 70 75 | |
| TTA CAG GCA CAG AAG CTG AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC | 286 |
| Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu | |
| 80 85 90 95 | |
| TGT ATT TCC AAT GGT AAT TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC | 334 |
| Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser | |
| 100 105 110 | |
| CAC ATA ACC ACA AAA TCA ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC | 382 |
| His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser | |
| 115 120 125 | |
| CCA CTG CTG GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA | 430 |
| Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu | |
| 130 135 140 | |
| ACA GAA ACA TCA TAG CTGCATTAAA AAAATACAAT ATGGACATGT AAAAAGACAA | 485 |
| Thr Glu Thr Ser * | |
| 145 | |

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AAACCAAGTT ATCTGTTTCC TGTTCTCTTG TATAGCTGAA ATTCCAGTTT AGGAGCTCAG      545
TTGAGAAAACA GTTCCATTCA ACTGGAACAT TTTTTTTTTT CCTTTTAAGA AAGCTTCTTG      605
TGATCCTTCG GGGCTTCTGT GAAAAACCTG ATGCAGTGCT CCATCCAAAC TCAGAAGGCT      665
TTGGGATATG CTGTATTTTA AAGGGACAGT TTGTAAGTTG GGCTGTAAAG CAAACTGGGG      725
CTGTGTTTTT GATGATGATG ATCATCATGA TCATGATNNN NNNNNNNNNN NNNNNNNNNN      785
NNNNNNNNNN NNNNNNGATT TTAACAGTTT TACTTCTGGC CTTTCCTAGC TAGAGAAGGA      845
GTTAATATTT CTAAGGTAAC TCCCATATCT CCTTTAATGA CATTGATTTC TAATGATATA      905
AATTCAGCC TACATTGATG CCAAGCTTTT TTGCCACAAA GAAGATTCTT ACCAAGAGTG      965
GGCTTTGTGG AAACAGCTGG TACTGATGTT CACCTTTATA TATGTACTAG CATTTTCCAC     1025
GCTGATGTTT ATGTACTGTA AACAGTTCTG CACTCTTGTA CAAAAGAAAA     1075

```

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp
 1          5          10          15
Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp
          20          25          30
Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr
          35          40          45
Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly
          50          55          60
Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu
          65          70          75          80
Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys
          85          90          95
Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His
          100          105          110
Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro
          115          120          125
Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr
          130          135          140
Glu Thr Ser *
145

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(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..428

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..1059
- (D) OTHER INFORMATION: /note= "1 to 1059 is 1272 to 2330

of Figure 5 Hsgr-9"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

| | |
|---|-----|
| AG TGC TTG AAA TTT TTG AAT TTC TTC AAG GAC AAT ACA TGT CTT AAA | 47 |
| Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys | |
| 1 5 10 15 | |
| AAT GCA ATT CAA GCC TTT GGC AAT GGC TCC GAT GTG ACC GTG TGG CAG | 95 |
| Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln | |
| 20 25 30 | |
| CCA GCC TTC CCA GTA CAG ACC ACC ACT GCC ACT ACC ACC ACT GCC CTC | 143 |
| Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu | |
| 35 40 45 | |
| CGG GTT AAG AAC AAG CCC CTG GGG CCA GCA GGG TCT GAG AAT GAA ATT | 191 |
| Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile | |
| 50 55 60 | |
| CCC ACT CAT GTT TTG CCA CCG TGT GCA AAT TTA CAG GCA CAG AAG CTG | 239 |
| Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu | |
| 65 70 75 | |
| AAA TCC AAT GTG TCG GGC AAT ACA CAC CTC TGT ATT TCC AAT GGT AAT | 287 |
| Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn | |
| 80 85 90 95 | |
| TAT GAA AAA GAA GGT CTC GGT GCT TCC AGC CAC ATA ACC ACA AAA TCA | 335 |
| Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser | |
| 100 105 110 | |
| ATG GCT GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG GTC CTG GTG | 383 |
| Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val | |
| 115 120 125 | |
| GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA ACA TCA TAG | 428 |
| Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser * | |
| 130 135 140 | |
| CTGCATTAAA AAAATACAAT ATGGACATGT AAAAAGACAA AAACCAAGTT ATCTGTTTCC | 488 |
| TGTTCTCTTG TATAGCTGAA ATTCCAGTTT AGGAGCTCAG TTGAGAAACA GTTCCATTCA | 548 |
| ACTGGAACAT TTTTTTTTTT TCCTTTTAAG AAAGCTTCTT GTGATCCTTT GGGGCTTCTG | 608 |

```

TGAAAAACCT GATGCAGTGC TCCATCCAAA CTCAGAAGGC TTTGGGATAT GCTGTATTTT      668
AAAGGGACAG TTTGTAACTT GGGCTGTAAA GCAAAGTGGG GCTGTGTTTT CGATGATGAT      728
GATGATCATG ATGATGATCA TCATGATCAT GATGATGATC ATCATGATCA TGATGATGAT      788
TTTAACAGTT TTAATTCTGG CCTTTCCTAG CTAGAGAAGG AGTTAATATT TCTAAGGTAA      848
CTCCCATATC TCCTTTAATG ACATTGATTT CTAATGATAT AAATTTTCAGC CTACATTGAT      908
GCCAAGCTTT TTTGCCACAA AGAAGATTCT TACCAAGAGT GGGCTTTGTG GAAACAGCTG      968
GTACTGATGT TCACCTTTAT ATATGTACTA GCATTTTCCA CGCTGATGTT TATGTACTGT     1028
AAACAGTTCT GCACTCTTGT ACAAAGAAA A                                     1059

```

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 142 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn
 1           5           10
Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro
          20           25           30
Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg
          35           40           45
Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro
          50           55           60
Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys
          65           70           75           80
Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr
          85           90           95
Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met
          100          105          110
Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val
          115          120          125
Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser *
          130          135          140

```

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

| | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ser | Cys | Ser | Thr | Lys | Tyr | Arg | Thr | Leu |
| 1 | | | | 5 | | | | | 10 |

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

| | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Lys | Arg | Gly | Met | Lys | Lys | Glu | Lys | Asn |
| 1 | | | | 5 | | | | | 10 |

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

| | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Glu | Asp | Ser | Pro | Tyr | Glu | Pro | Val |
| 1 | | | | 5 | | | | | 10 |

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ser | Tyr | Glu | Glu | Arg | Glu | Arg | Pro | Asn |
| 1 | | | | 5 | | | | | 10 |

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ala | Pro | Pro | Val | Gln | Thr | Thr | Thr | Ala | Thr | Thr | Thr | Thr |
| 1 | | | | 5 | | | | | 10 | | | | |

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTGTTTGAAT TTGCAGGACT C

21

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTCCTCTCTA AGCTTCTAAC CACAGCTTGG AGGAGC

36

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
CTCCTCTCTA AGCTTCTATG GGCTCAGACC ACAGCTT 37

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
CTCCTCTCTA AGCTTCTACT TGTCATCGTC GTCCTTGTAG TCACCACAGC TTGGAGGAGC 60

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
CTCCTCTCTA AGCTTCTACT TGTCATCGTC GTCCTTGTAG TCTGGCTCAG ACCACAGCTT 60

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1587..2978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
CATGAAGAAA CCTCAGTAAG TCTCAGACTT GGCCCAAAGG AGCCCAACTA GTTACTCCCT 60
GGTCTGTTAC AGAGGATCTG GCTATTACAC TCAACAGCAA AAATTCAATT CAATCCCGCT 120
AAAGATATAA GAATCACTAG GAAKAATAAG CCAGAACTCA AGACAGAAAT AGCATTAAGT 180

| | | | | | | |
|---|------------|------------|-------------------------------------|------------|------------|------|
| AGTTCCTTCA | GTACAGTGAG | CAGAAGCTGG | CCACTCTACG | ACTCTAWAAG | ACTCAGAAAA | 240 |
| GCTTACTAGG | GACCWCTGGG | CATWCCGGTG | TCCTATGTGG | GGATTTCGTA | ACGTCTTTGA | 300 |
| GTCAGAAAGCT | GCCCTCAAAA | TAGTTTCTTC | TCAAAACGGT | TTCAGGCTTT | GTTAGAAAGG | 360 |
| GAAGACTTCA | CTGCCACTTT | ACCCAGATCA | TCTACCCCAT | CCTTGGAATG | AATGGGGAAG | 420 |
| CTTCAGCCAC | CCTACCAGGC | TCCTAAAATC | ACCAACTTGA | GAGAAAAACT | ATAACGTTGC | 480 |
| TCTACCAGTA | CTTCAGGAGG | TTAAAGAAAG | TCACAGAAAG | AAAGAACTCT | GGGGAAAACA | 540 |
| GTCAAATTCG | GCTATTAAGA | CATTAGTTAC | AGGCCCCCTGT | ACCTCTCCTC | TAGAAACCCT | 600 |
| GGGAGTACAC | CCGCAGAGGA | GAGAGAGCCC | AAGCCACCAA | GCAAAGTCAA | CCAATCTGGC | 660 |
| AAAGGGGCGT | CCCACTGCGG | CTTTCAGTCC | AAGAAGTGGA | TCCTGCTGGT | TCGCAGTCTC | 720 |
| TCTTCTATCT | CCTCACTTCC | TATTTACCCT | TTGAAGTGGG | TACTGAATAG | CCCGTTCCCA | 780 |
| AGCAGAGGCC | CTTTGTATAC | GGGGTGCTAC | AGTCGCCTGG | TGGAAACACC | TTGGCAGAGT | 840 |
| TGTTTGGTGC | CAGGATGGGC | CACTGAAGGC | ATCTGCTGTG | GACACACACA | CACACACACA | 900 |
| CACACACACA | CACACACACA | GAGAGAGGAG | AGAGAAAAGAC | ACACGCACGC | AGAGACACAC | 960 |
| GGTCACTGGA | ATTCCATTAG | AAAAAAGTGA | GCCGAGCAAG | GGTTAGCGGG | AGAAGATTTT | 1020 |
| TTTGAATCTT | GTCTTCGTCT | TGGTGCGAAA | GAAGCGACTC | CAGTCTCTCG | TCCTCGAAGC | 1080 |
| TCCGACTGGA | TTGTTCTTGG | GCGCTGACAC | CCGTCTGTGG | ATTTCTTTTC | TATTTGCATT | 1140 |
| TTATTCCGAC | CCCCTCCCTC | GCCGCTTCCT | TCCAGCCCTT | CACTCGCAAA | TCGCCTCTCT | 1200 |
| CCCCACCTCC | CCAGGCCCTT | CCTGGGAAGC | GCAGGGGAAT | TGGACCCGCG | GGGACTCACG | 1260 |
| CCTTCCCAGG | CGATTGGAGG | GGAGGGCTGA | CCCCAGGACT | GGGCTGTTGG | CTTAGAAAGC | 1320 |
| CGATACACAG | ATACGCGTAT | ATTTGATTGT | AGCGGGCAAG | GGGGGCGTCG | AGAGGCAGCA | 1380 |
| GCCCCATCGC | CGCCTCTCAC | CCCACCCCTT | CCAGCCAGAG | GCGAGAATCG | CAGGACTCGG | 1440 |
| GATCTTCATC | GGGTGGACTA | GCTGGGATCT | CCGCATTGGA | TTTGGGGCTG | ATTACCACTG | 1500 |
| CTTGGCTATT | ATTATTGTTG | TTGTTACTAC | TATTATTTTT | TTTTACCCAA | GGGAGAAAGA | 1560 |
| CAAAAAAACG | GTGGGATTTA | TTTAAC | ATG ATC TTG GCA AAC GTC TTC TGC CTC | | | 1613 |
| | | | Met Ile Leu Ala Asn Val Phe Cys Leu | | | |
| | | | 1 | 5 | | |
| TTC TTC TTT CTA GAC GAC ACC CTC CGC TCT TTG GCC AGC CCT TCC TCC | | | | | | 1661 |
| Phe Phe Phe Leu Asp Asp Thr Leu Arg Ser Leu Ala Ser Pro Ser Ser | | | | | | |
| 10 | 15 | 20 | 25 | | | |
| CTG CAG GGC CCC GAG CTC CAC GGC TGG CGC CCC CCA GTG GAC TGT GTC | | | | | | 1709 |
| Leu Gln Gly Pro Glu Leu His Gly Trp Arg Pro Pro Val Asp Cys Val | | | | | | |
| | 30 | 35 | 40 | | | |
| CGG GCC AAT GAG CTG TGT GCC GCC GAA TCC AAC TGC AGC TCT CGC TAC | | | | | | 1757 |
| Arg Ala Asn Glu Leu Cys Ala Ala Glu Ser Asn Cys Ser Ser Arg Tyr | | | | | | |
| | 45 | 50 | 55 | | | |
| CGC ACT CTG CGG CAG TGC CTG GCA GGC CGC GAC CGC AAC ACC ATG CTG | | | | | | 1805 |
| Arg Thr Leu Arg Gln Cys Leu Ala Gly Arg Asp Arg Asn Thr Met Leu | | | | | | |

| 60 | | | | | 65 | | | | | 70 | | | | | | |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| GCC Ala | AAC Asn 75 | AAG Lys | GAG Glu | TGC Cys | CAG Gln 80 | GCG Ala | GCC Ala | TTG Leu | GAG Glu | GTC Val | TTG Leu 85 | CAG Gln | GAG Glu | AGC Ser | CCG Pro | 1853 |
| CTG Leu 90 | TAC Tyr | GAC Asp | TGC Cys | CGC Arg | TGC Cys 95 | AAG Lys | CGG Arg | GGC Gly | ATG Met | AAG Lys 100 | AAG Lys | GAG Glu | CTG Leu | CAG Gln | TGT Cys 105 | 1901 |
| CTG Leu | CAG Gln | ATC Ile | TAC Tyr | TGG Trp 110 | AGC Ser | ATC Ile | CAC His | CTG Leu | GGG Gly 115 | CTG Leu | ACC Thr | GAG Glu | GGT Gly | GAG Glu 120 | GAG Glu | 1949 |
| TTC Phe | TAC Tyr | GAA Glu 125 | GCC Ala | TCC Ser | CCC Pro | TAT Tyr | GAG Glu | CCG Pro 130 | GTG Val | ACC Thr | TCC Ser | CGC Arg | CTC Leu 135 | TCG Ser | GAC Asp | 1997 |
| ATC Ile | TTC Phe 140 | AGG Arg | CTT Leu | GCT Ala | TCA Ser | ATC Ile | TTC Phe 145 | TCA Ser | GGG Gly | ACA Thr | GGG Gly | GCA Ala 150 | GAC Asp | CCG Pro | GTG Val | 2045 |
| GTC Val | AGC Ser 155 | GCC Ala | AAG Lys | AGC Ser | AAC Asn | CAT His 160 | TGC Cys | CTG Leu | GAT Asp | GCT Ala | GCC Ala 165 | AAG Lys | GCC Ala | TGC Cys | AAC Asn | 2093 |
| CTG Leu 170 | AAT Asn | GAC Asp | AAC Asn | TGC Cys | AAG Lys 175 | AAG Lys | CTG Leu | CGC Arg | TCC Ser | TCC Ser 180 | TAC Tyr | ATC Ile | TCC Ser | ATC Ile | TGC Cys 185 | 2141 |
| AAC Asn | CGC Arg | GAG Glu | ATC Ile | TCG Ser 190 | CCC Pro | ACC Thr | GAG Glu | CGC Arg | TGC Cys 195 | AAC Asn | CGC Arg | CGC Arg | AAG Lys | TGC Cys 200 | CAC His | 2189 |
| AAG Lys | GCC Ala | CTG Leu | CGC Arg 205 | CAG Gln | TTC Phe | TTC Phe | GAC Asp 210 | CGG Arg | GTG Val | CCC Pro | AGC Ser | GAG Glu | TAC Tyr 215 | ACC Thr | TAC Tyr | 2237 |
| CGC Arg | ATG Met | CTC Leu 220 | TTC Phe | TGC Cys | TCC Ser | TGC Cys | CAA Gln 225 | GAC Asp | CAG Gln | GCG Ala | TGC Cys 230 | GCT Ala | GAG Glu | CGC Arg | CGC Arg | 2285 |
| CGG Arg | CAA Gln 235 | ACC Thr | ATC Ile | CTG Leu | CCC Pro | AGC Ser 240 | TGC Cys | TCC Ser | TAT Tyr | GAG Glu | GAC Asp 245 | AAG Lys | GAG Glu | AAG Lys | CCC Pro | 2333 |
| AAC Asn 250 | TGC Cys | CTG Leu | GAC Asp | CTG Leu | CGT Arg 255 | GGC Gly | GTG Val | TGC Cys | CGG Arg | ACT Thr 260 | GAC Asp | CAC His | CTG Leu | TGT Cys | CGG Arg 265 | 2381 |
| TCC Ser | CGG Arg | CTG Leu | GCC Ala | GAC Asp 270 | TTC Phe | CAT His | GCC Ala | AAT Asn | TGT Cys 275 | CGA Arg | GCC Ala | TCC Ser | TAC Tyr | CAG Gln 280 | ACG Thr | 2429 |
| GTC Val | ACC Thr | AGC Ser | TGC Cys 285 | CCT Pro | GCG Ala | GAC Asp | AAT Asn | TAC Tyr 290 | CAG Gln | GCG Ala | TGT Cys | CTG Leu | GGC Gly 295 | TCT Ser | TAT Tyr | 2477 |
| GCT Ala | GGC Gly | ATG Met 300 | ATT Ile | GGG Gly | TTT Phe | GAC Asp | ATG Met 305 | ACA Thr | CCT Pro | AAC Asn | TAT Tyr 310 | GTG Val | GAC Asp | TCC Ser | AGC Ser | 2525 |
| CCC Pro | ACT Thr | GGC Gly | ATC Ile | GTG Val | GTG Val | TCC Ser | CCC Pro | TGG Trp | TGC Cys | AGC Ser | TGT Cys | CGT Arg | GGC Gly | AGC Ser | GGG Gly | 2573 |

| 315 | 320 | 325 | |
|---|-----|-----|------|
| AAC ATG GAG GAG GAG TGT GAG AAG TTC CTC AGG GAC TTC ACC GAG AAC Asn Met Glu Glu Glu Cys Glu Lys Phe Leu Arg Asp Phe Thr Glu Asn 330 335 340 345 | | | 2621 |
| CCA TGC CTC CGG AAC GCC ATC CAG GCC TTT GGC AAC GGC ACG AAC GTG Pro Cys Leu Arg Asn Ala Ile Gln Ala Phe Gly Asn Gly Thr Asn Val 350 355 360 | | | 2669 |
| AAC GTG TCC CCA AAA GGC CCC TCG TTC CAG GCC ACC CAG GCC CCT CGG Asn Val Ser Pro Lys Gly Pro Ser Phe Gln Ala Thr Gln Ala Pro Arg 365 370 375 | | | 2717 |
| GTG GAG AAG ACG CCT TCT TTG CCA GAT GAC CTC AGT GAC AGT ACC AGC Val Glu Lys Thr Pro Ser Leu Pro Asp Asp Leu Ser Asp Ser Thr Ser 380 385 390 | | | 2765 |
| TTG GGG ACC AGT GTC ATC ACC ACC TGC ACG TCT GTC CAG GAG CAG GGG Leu Gly Thr Ser Val Ile Thr Thr Cys Thr Ser Val Gln Glu Gln Gly 395 400 405 | | | 2813 |
| CTG AAG GCC AAC AAC TCC AAA GAG TTA AGC ATG TGC TTC ACA GAG CTC Leu Lys Ala Asn Asn Ser Lys Glu Leu Ser Met Cys Phe Thr Glu Leu 410 415 420 425 | | | 2861 |
| ACG ACA AAT ATC ATC CCA GGG AGT AAC AAG GTG ATC AAA CCT AAC TCA Thr Thr Asn Ile Ile Pro Gly Ser Asn Lys Val Ile Lys Pro Asn Ser 430 435 440 | | | 2909 |
| GGC CCC AGC AGA GCC AGA CCG TCG GCT GCC TTG ACC GTG CTG TCT GTC Gly Pro Ser Arg Ala Arg Pro Ser Ala Ala Leu Thr Val Leu Ser Val 445 450 455 | | | 2957 |
| CTG ATG CTG AAA CTG GCC TTG TAGGCTGTGG GAACCGAGTC AGAAGATTTT Leu Met Leu Lys Leu Ala Leu | | | 3008 |
| 460 | | | |
| TGAAAGCTAC GCAGACAAGA ACAGCCGCCT GACGAAATGG AAACACACAC AGACACACAC | | | 3068 |
| ACACCTTGCA AAAAAAAAAAT TGTTTTTCCC ACCTTGTCGC TGAACCTGTC TCCTCCCAGG | | | 3128 |
| TTTCTTCTCT GGAGAAGTTT TTGTAAACCA AACAGACAAG CAGGCAGGCA GCCTGAGAGC | | | 3188 |
| TGGCCCAGGG GTCCCCTGGC AGGGGAAACT CTGGTGCCGG GGAGGGCACG AGGCTCTAGA | | | 3248 |
| AATGCCCTTC ACTTTCTCCT GGTGTTTTTC TCTCTGGACC CTTCTGAAGC AGAGACCGGA | | | 3308 |
| CAAGAGCCTG CAGCGGAAGG GACTCTGGGC TGTGCCTGAG GCTGGCTGGG GGCAGGACAA | | | 3368 |
| CACAGCTGCT TCCCCAGGCT GCCCACTCTG GGGACCCGCT GGGGGCTGGC AGAGGGCATC | | | 3428 |
| GGTCAGCGGG GCAGCGGGGC TGGCCATGAG GGTCCACCTT CAGCCCTTTG GCTTCAAGGA | | | 3488 |
| TGGAGATGGT TTTGCCCTCC CTCTCTGCCC TCGGGTGGGG CTGGTGGGTC TGCAGCTGGT | | | 3548 |
| GTGGGAACTT CCCCACGGAT GGCGGTGGAG GGGGTTCGCA CCGTGCTGGG CTCCCCCTGA | | | 3608 |
| CTGTAGCACG GAGTGTGGG GCTGGGGGCC AGCTCCAGGA GGGCTTGAGA GCTCAGCCTG | | | 3668 |
| CCTGGGAGAG CCCTTGTGGC GAGGCATTAA AACTTGGGCA CCAGCTTCTT TCTCGGTGGC | | | 3728 |
| AGAAATTTTG AAGTCAGAGA GAAACGGTCC TTTGTTGGCT TCTTTGCTTT CTCGTGGGTC | | | 3788 |

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CTTTGGCAGG CCTCCCTTTG GGGAGAGGGA GGGGAGAGAC CACAGCCGGG TGTGTGTCTG      3848
CAGCACCGTG GGCCCTCAAG CTTTCCTGCT GTCTTCTCCC TCCTCCTCCT TTCCCCTTTC      3908
TCTTTCCTCA TTTCCTAGAC GTACGTCAAC TGTATGTACA TACCGGGGCT CCTCTCCTAA      3968
CATATATGTA TATACACATC CATATACATA TATTGTGTGG TTTCCCCTTT CTTTCCTTTT      4028
TTTAAGCAAC AAAACTATGG AAATAATACC CCAACAGATG AGCGAAAATG TATTATTGTA      4088
AAGTTTATTT TTTTAAATAC TGTTGTCTAT AATGGGGAAA AAGGACATTG GCCCCGCAGT      4148
GCCCTGCCCC AGTCAGCCTG GCTGGGCTCT GGTGGGGGCT CCTGATCCGC ATCCAAGCTT      4208
AACCAAGGCT CCAATAAACG TGCG                                          4232

```

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 464 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

Met Ile Leu Ala Asn Val Phe Cys Leu Phe Phe Phe Leu Asp Asp Thr
 1               5              10      15
Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Pro Glu Leu His
                20              25      30
Gly Trp Arg Pro Pro Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala
              35              40      45
Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu
          50              55      60
Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala
 65              70      75      80
Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys
              85              90      95
Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile
              100             105      110
His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr
              115             120      125
Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile
          130             135      140
Phe Ser Gly Thr Gly Ala Asp Pro Val Val Ser Ala Lys Ser Asn His
145             150      155      160
Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys
              165             170      175
Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr
          180             185      190

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Arg | Cys | Asn | Arg | Arg | Lys | Cys | His | Lys | Ala | Leu | Arg | Gln | Phe | Phe |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Asp | Arg | Val | Pro | Ser | Glu | Tyr | Thr | Tyr | Arg | Met | Leu | Phe | Cys | Ser | Cys |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Gln | Asp | Gln | Ala | Cys | Ala | Glu | Arg | Arg | Arg | Gln | Thr | Ile | Leu | Pro | Ser |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Cys | Ser | Tyr | Glu | Asp | Lys | Glu | Lys | Pro | Asn | Cys | Leu | Asp | Leu | Arg | Gly |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Val | Cys | Arg | Thr | Asp | His | Leu | Cys | Arg | Ser | Arg | Leu | Ala | Asp | Phe | His |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ala | Asn | Cys | Arg | Ala | Ser | Tyr | Gln | Thr | Val | Thr | Ser | Cys | Pro | Ala | Asp |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Asn | Tyr | Gln | Ala | Cys | Leu | Gly | Ser | Tyr | Ala | Gly | Met | Ile | Gly | Phe | Asp |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Met | Thr | Pro | Asn | Tyr | Val | Asp | Ser | Ser | Pro | Thr | Gly | Ile | Val | Val | Ser |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Pro | Trp | Cys | Ser | Cys | Arg | Gly | Ser | Gly | Asn | Met | Glu | Glu | Glu | Cys | Glu |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Lys | Phe | Leu | Arg | Asp | Phe | Thr | Glu | Asn | Pro | Cys | Leu | Arg | Asn | Ala | Ile |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Gln | Ala | Phe | Gly | Asn | Gly | Thr | Asn | Val | Asn | Val | Ser | Pro | Lys | Gly | Pro |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Ser | Phe | Gln | Ala | Thr | Gln | Ala | Pro | Arg | Val | Glu | Lys | Thr | Pro | Ser | Leu |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Pro | Asp | Asp | Leu | Ser | Asp | Ser | Thr | Ser | Leu | Gly | Thr | Ser | Val | Ile | Thr |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Thr | Cys | Thr | Ser | Val | Gln | Glu | Gln | Gly | Leu | Lys | Ala | Asn | Asn | Ser | Lys |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Glu | Leu | Ser | Met | Cys | Phe | Thr | Glu | Leu | Thr | Thr | Asn | Ile | Ile | Pro | Gly |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Ser | Asn | Lys | Val | Ile | Lys | Pro | Asn | Ser | Gly | Pro | Ser | Arg | Ala | Arg | Pro |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Ser | Ala | Ala | Leu | Thr | Val | Leu | Ser | Val | Leu | Met | Leu | Lys | Leu | Ala | Leu |
| | 450 | | | | | 455 | | | | | 460 | | | | |

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1991 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 203..1402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

| | |
|---|-----|
| CAAGTCAAAG GTTTAATCAT GATCCAAGAG CCCAGAGAGA CTTTAGGACA ATAATAGGAA | 60 |
| TAAAGCAAGG CCCACAGGCT CCAGCTCCTG ATGCCCAGAT GTTCGGCAGG ATCCGGGGAC | 120 |
| AGGGCAGTGC AGGCAGTAGT TTTCCATCCT CCATCCAGGG GAGGAGCGAG GGGAGCGCGG | 180 |
| AGCCCGGCGC CTACAGCTCG CC ATG GTG CGC CCC CTG AAC CCG CGA CCG CTG | 232 |
| Met Val Arg Pro Leu Asn Pro Arg Pro Leu | |
| 1 5 10 | |
| CCG CCC GTA GTC CTG ATG TTG CTG CTG CTG CTG CCG CCG TCG CCG CTG | 280 |
| Pro Pro Val Val Leu Met Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu | |
| 15 20 25 | |
| CCT CTC GCA GCC GGA GAC CCC CTT CCC ACA GAA AGC CGA CTC ATG AAC | 328 |
| Pro Leu Ala Ala Gly Asp Pro Leu Pro Thr Glu Ser Arg Leu Met Asn | |
| 30 35 40 | |
| AGC TGT CTC CAG GCC AGG AGG AAG TGC CAG GCT GAT CCC ACC TGC AGT | 376 |
| Ser Cys Leu Gln Ala Arg Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser | |
| 45 50 55 | |
| GCT GCC TAC CAC CAC CTG GAT TCC TGC ACC TCT AGC ATA AGC ACC CCA | 424 |
| Ala Ala Tyr His His Leu Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro | |
| 60 65 70 | |
| CTG CCC TCA GAG GAG CCT TCG GTC CCT GCT GAC TGC CTG GAG GCA GCA | 472 |
| Leu Pro Ser Glu Glu Pro Ser Val Pro Ala Asp Cys Leu Glu Ala Ala | |
| 75 80 85 90 | |
| CAG CAA CTC AGG AAC AGC TCT CTG ATA GGC TGC ATG TGC CAC CGG CGC | 520 |
| Gln Gln Leu Arg Asn Ser Ser Leu Ile Gly Cys Met Cys His Arg Arg | |
| 95 100 105 | |
| ATG AAG AAC CAG GTT GCC TGC TTG GAC ATC TAT TGG ACC GTT CAC CGT | 568 |
| Met Lys Asn Gln Val Ala Cys Leu Asp Ile Tyr Trp Thr Val His Arg | |
| 110 115 120 | |
| GCC CGC AGC CTT GGT AAC TAT GAG CTG GAT GTC TCC CCC TAT GAA GAC | 616 |
| Ala Arg Ser Leu Gly Asn Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp | |
| 125 130 135 | |
| ACA GTG ACC AGC AAA CCC TGG AAA ATG AAT CTC AGC AAA CTG AAC ATG | 664 |
| Thr Val Thr Ser Lys Pro Trp Lys Met Asn Leu Ser Lys Leu Asn Met | |
| 140 145 150 | |
| CTC AAA CCA GAC TCA GAC CTC TGC CTC AAG TTT GCC ATG CTG TGT ACT | 712 |
| Leu Lys Pro Asp Ser Asp Leu Cys Leu Lys Phe Ala Met Leu Cys Thr | |
| 155 160 165 170 | |
| CTC AAT GAC AAG TGT GAC CGG CTG CGC AAG GCC TAC GGG GAG GCG TGC | 760 |
| Leu Asn Asp Lys Cys Asp Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys | |
| 175 180 185 | |
| TCC GGG CCC CAC TGC CAG CGC CAC GTC TGC CTC AGG CAG CTG CTC ACT | 808 |
| Ser Gly Pro His Cys Gln Arg His Val Cys Leu Arg Gln Leu Leu Thr | |
| 190 195 200 | |

| | | | | | | | | | | | | | | | | |
|------------|------------|-----|------------|-----|------------|----------------------------------|------------|-----|-------------|-----|-----|-----|-----|-----|-----|------|
| TTC | TTC | GAG | AAG | GCC | GCC | GAG | CCC | CAC | GCG | CAG | GGC | CTG | CTA | CTG | TGC | 856 |
| Phe | Phe | Glu | Lys | Ala | Ala | Glu | Pro | His | Ala | Gln | Gly | Leu | Leu | Leu | Cys | |
| | | 205 | | | | | 210 | | | | | 215 | | | | |
| CCA | TGT | GCC | CCC | AAC | GAC | CGG | GGC | TGC | GGG | GAG | CGC | CGG | CGC | AAC | ACC | 904 |
| Pro | Cys | Ala | Pro | Asn | Asp | Arg | Gly | Cys | Gly | Glu | Arg | Arg | Arg | Asn | Thr | |
| | 220 | | | | | 225 | | | | | 230 | | | | | |
| ATC | GCC | CCC | AAC | TGC | GCG | CTG | CCG | CCT | GTG | GCC | CCC | AAC | TGC | CTG | GAG | 952 |
| Ile | Ala | Pro | Asn | Cys | Ala | Leu | Pro | Pro | Val | Ala | Pro | Asn | Cys | Leu | Glu | |
| 235 | | | | | 240 | | | | | 245 | | | | | 250 | |
| CTG | CGG | CGC | CTC | TGC | TTC | TCC | GAC | CCG | CTT | TGC | AGA | TCA | CGC | CTG | GTG | 1000 |
| Leu | Arg | Arg | Leu | Cys | Phe | Ser | Asp | Pro | Leu | Cys | Arg | Ser | Arg | Leu | Val | |
| | | | 255 | | | | | | 260 | | | | | 265 | | |
| GAT | TTC | CAG | ACC | CAC | TGC | CAT | CCC | ATG | GAC | ATC | CTA | GGA | ACT | TGT | GCA | 1048 |
| Asp | Phe | Gln | Thr | His | Cys | His | Pro | Met | Asp | Ile | Leu | Gly | Thr | Cys | Ala | |
| | | | 270 | | | | | 275 | | | | | 280 | | | |
| ACA | GAG | CAG | TCC | AGA | TGT | CTA | CGA | GCA | TAC | CTG | GGG | CTG | ATT | GGG | ACT | 1096 |
| Thr | Glu | Gln | Ser | Arg | Cys | Leu | Arg | Ala | Tyr | Leu | Gly | Leu | Ile | Gly | Thr | |
| | 285 | | | | | | 290 | | | | | 295 | | | | |
| GCC | ATG | ACC | CCC | AAC | TTT | GCC | AGC | AAT | GTC | AAC | ACC | AGT | GTT | GCC | TTA | 1144 |
| Ala | Met | Thr | Pro | Asn | Phe | Ala | Ser | Asn | Val | Asn | Thr | Ser | Val | Ala | Leu | |
| | 300 | | | | | 305 | | | | | 310 | | | | | |
| AGC | TGC | ACC | TGC | CGA | GGC | AGT | GGC | AAC | CTG | CAG | GAG | GAG | TGT | GAA | ATG | 1192 |
| Ser | Cys | Thr | Cys | Arg | Gly | Ser | Gly | Asn | Leu | Gln | Glu | Glu | Cys | Glu | Met | |
| 315 | | | | | 320 | | | | | 325 | | | | | 330 | |
| CTG | GAA | GGG | TTC | TTC | TCC | CAC | AAC | CCC | TGC | CTC | ACG | GAG | GCC | ATT | GCA | 1240 |
| Leu | Glu | Gly | Phe | Phe | Ser | His | Asn | Pro | Cys | Leu | Thr | Glu | Ala | Ile | Ala | |
| | | | 335 | | | | | | 340 | | | | | 345 | | |
| GCT | AAG | ATG | CGT | TTT | CAC | AGC | CAA | CTC | TTC | TCC | CAG | GAC | TGG | CCA | CAC | 1288 |
| Ala | Lys | Met | Arg | Phe | His | Ser | Gln | Leu | Phe | Ser | Gln | Asp | Trp | Pro | His | |
| | | | 350 | | | | | 355 | | | | | 360 | | | |
| CCT | ACC | TTT | GCT | GTG | ATG | GCA | CAC | CAG | AAT | GAA | AAC | CCT | GCT | GTG | AGG | 1336 |
| Pro | Thr | Phe | Ala | Val | Met | Ala | His | Gln | Asn | Glu | Asn | Pro | Ala | Val | Arg | |
| | | 365 | | | | | 370 | | | | | 375 | | | | |
| CCA | CAG | CCC | TGG | GTG | CCC | TCT | CTT | TTC | TCC | TGC | ACG | CTT | CCC | TTG | ATT | 1384 |
| Pro | Gln | Pro | Trp | Val | Pro | Ser | Leu | Phe | Ser | Cys | Thr | Leu | Pro | Leu | Ile | |
| | 380 | | | | | 385 | | | | | 390 | | | | | |
| CTG | CTC | CTG | AGC | CTA | TGG | TAGCTGGACT TCCCCAGGGC CCTCTTCCCC | | | | | | | | | | 1432 |
| Leu | Leu | Leu | Ser | Leu | Trp | 400 | | | | | | | | | | |
| 395 | | | | | | | | | | | | | | | | |
| TCCACCACAC | CCAGGTGGAC | | TTGCAGCCCA | | CAAGGGGTGA | | GGAAAGGACA | | GCAGCAGGAA | | | | | | | 1492 |
| GGAGGTGCAG | TGCGCAGATG | | AGGGCACAGG | | AGAAGCTAAG | | GGTTATGACC | | TCCAGATCCT | | | | | | | 1552 |
| TACTGGTCCA | GTCCTCATTC | | CCTCCACCCC | | ATCTCCACTT | | CTGATTCATG | | CTGCCCCCTCC | | | | | | | 1612 |
| TTGGTGGCCA | CAATTTAGCC | | ATGTCATCTG | | GTGGTGACCA | | GCTCCACCAA | | GCCCCTTTGT | | | | | | | 1672 |
| GAGCCCTTCC | TCTTGACTAC | | CAGGATCACC | | AGAATCTAAT | | AAGTTAGCCT | | TTCTCTATTG | | | | | | | 1732 |
| CATTCCAGAT | TAGGGTTAGG | | GTAGGGAGGA | | CTGGGTGTTC | | TGAGGCAGCC | | TAGAAAGTCA | | | | | | | 1792 |

TTCTCCTTTG TGAAGAAGGC TCCTGCCCCC TCGTCTCCTC CTCTGAGTGG AGGATGGAAA 1852
 ACTACTGCCT GCACTGCCCT GTCCCCGGAT CCTGCCGAAC ATCTGGGCAT CAGGAGCTGG 1912
 AGCCTGTGGG CCTTGCTTTA TTCCTATTAT TGTCTCTAAAG TCTCTCTGGG CTCTTGGATC 1972
 ATGATTAAAC CTTTGACTG 1991

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Arg | Pro | Leu | Asn | Pro | Arg | Pro | Leu | Pro | Pro | Val | Val | Leu | Met | 1 | 5 | 10 | 15 |
| Leu | Leu | Leu | Leu | Leu | Pro | Pro | Ser | Pro | Leu | Pro | Leu | Ala | Ala | Gly | Asp | 20 | 25 | 30 | |
| Pro | Leu | Pro | Thr | Glu | Ser | Arg | Leu | Met | Asn | Ser | Cys | Leu | Gln | Ala | Arg | 35 | 40 | 45 | |
| Arg | Lys | Cys | Gln | Ala | Asp | Pro | Thr | Cys | Ser | Ala | Ala | Tyr | His | His | Leu | 50 | 55 | 60 | |
| Asp | Ser | Cys | Thr | Ser | Ser | Ile | Ser | Thr | Pro | Leu | Pro | Ser | Glu | Glu | Pro | 65 | 70 | 75 | 80 |
| Ser | Val | Pro | Ala | Asp | Cys | Leu | Glu | Ala | Ala | Gln | Gln | Leu | Arg | Asn | Ser | 85 | 90 | 95 | |
| Ser | Leu | Ile | Gly | Cys | Met | Cys | His | Arg | Arg | Met | Lys | Asn | Gln | Val | Ala | 100 | 105 | 110 | |
| Cys | Leu | Asp | Ile | Tyr | Trp | Thr | Val | His | Arg | Ala | Arg | Ser | Leu | Gly | Asn | 115 | 120 | 125 | |
| Tyr | Glu | Leu | Asp | Val | Ser | Pro | Tyr | Glu | Asp | Thr | Val | Thr | Ser | Lys | Pro | 130 | 135 | 140 | |
| Trp | Lys | Met | Asn | Leu | Ser | Lys | Leu | Asn | Met | Leu | Lys | Pro | Asp | Ser | Asp | 145 | 150 | 155 | 160 |
| Leu | Cys | Leu | Lys | Phe | Ala | Met | Leu | Cys | Thr | Leu | Asn | Asp | Lys | Cys | Asp | 165 | 170 | 175 | |
| Arg | Leu | Arg | Lys | Ala | Tyr | Gly | Glu | Ala | Cys | Ser | Gly | Pro | His | Cys | Gln | 180 | 185 | 190 | |
| Arg | His | Val | Cys | Leu | Arg | Gln | Leu | Leu | Thr | Phe | Phe | Glu | Lys | Ala | Ala | 195 | 200 | 205 | |
| Glu | Pro | His | Ala | Gln | Gly | Leu | Leu | Leu | Cys | Pro | Cys | Ala | Pro | Asn | Asp | 210 | 215 | 220 | |
| Arg | Gly | Cys | Gly | Glu | Arg | Arg | Arg | Asn | Thr | Ile | Ala | Pro | Asn | Cys | Ala | | | | |

| | | | |
|-----------------|-----------------------------|-------------------------|---------|
| 225 | 230 | 235 | 240 |
| Leu Pro Pro Val | Ala Pro Asn Cys Leu Glu | Leu Arg Arg Leu Cys Phe | |
| | 245 | 250 | 255 |
| Ser Asp Pro | Leu Cys Arg Ser Arg | Leu Val Asp Phe Gln Thr | His Cys |
| | 260 | 265 | 270 |
| His Pro Met Asp | Ile Leu Gly Thr Cys Ala Thr | Glu Gln Ser Arg Cys | |
| | 275 | 280 | 285 |
| Leu Arg Ala Tyr | Leu Gly Leu Ile Gly Thr Ala | Met Thr Pro Asn Phe | |
| | 290 | 295 | 300 |
| Ala Ser Asn Val | Asn Thr Ser Val Ala Leu | Ser Cys Thr Cys Arg Gly | |
| 305 | 310 | 315 | 320 |
| Ser Gly Asn Leu | Gln Glu Glu Cys Glu Met | Leu Glu Gly Phe Phe Ser | |
| | 325 | 330 | 335 |
| His Asn Pro | Cys Leu Thr Glu Ala Ile Ala | Ala Lys Met Arg Phe His | |
| | 340 | 345 | 350 |
| Ser Gln Leu Phe | Ser Gln Asp Trp Pro His Pro | Thr Phe Ala Val Met | |
| | 355 | 360 | 365 |
| Ala His Gln Asn | Glu Asn Pro Ala Val Arg Pro | Gln Pro Trp Val Pro | |
| | 370 | 375 | 380 |
| Ser Leu Phe Ser | Cys Thr Leu Pro Leu Ile Leu | Leu Leu Leu Ser Leu Trp | |
| 385 | 390 | 395 | 400 |

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2215 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 684..2063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

| | |
|---|-----|
| GCGGCCGCGT CGACCTTGAC CATGCAGACA CTTTTTCAGG CCTCTGTCTG GTGTGAAGTT | 60 |
| GGCAGATACA AGCAAGGCC GAAAGGGGTC TCAGCTTCTC TCTCCTGGGC CTCCTGGACT | 120 |
| GAGTTAGGCT TGCTTCTGGT TGTCTTCTAA AGGCACGGTG ATACAGAATG ATGAGACTAG | 180 |
| GCTGGAGGGG GCTTTCTGCT TCTCTGTGTG TGACCTTGAG TTATCTCCCT TCGTTGGATC | 240 |
| CGAGCTTTCC TGGAATATGA TGTTGAATAT GAATATGAGT TCTGCCTAAG GTCCAGACAG | 300 |
| GCTCTGAGGG TTAAGTACT TTTGGAGCCT TCAAATCAAT ACCTTGATG GAGTGGGGGT | 360 |
| TTGTCCAATG GGAGTTGAGG CAAGATCCCT TTGCATAAGC CTTGCCACAT CATGTTGAAG | 420 |

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|------|
| CCATGCCATT | CTGTCTGGAC | TATTGGCATC | TTACCTTTCC | AGCAGTTTCA | GTGAAGGCCT | 480 |
| TCCTGGATTT | ATCATTCCTGT | GTTCCACTGC | CTAGGATTGT | GCTCAAGAGG | AAATGAATGT | 540 |
| GAACCATGGT | TGTAGGGGAG | TATGGCCAAC | CAGGTTGGGT | CTGTGTTGAC | CTTGGTCTTG | 600 |
| GTGTTCTTTT | GTGTAAAGTG | GGTGAGAAGT | TCCTTCAAAC | CTTAGGCCTA | CATTGGGGTC | 660 |
| AGAGACTGTG | GTGGCCCTCA | TTC | ATG | CTT | GTC | 710 |
| | | Met | Leu | Val | Phe | |
| | | 1 | | | 5 | |
| GAC | GAA | ACC | CTC | CGC | TCT | 758 |
| Asp | Glu | Thr | Leu | Arg | Ser | |
| 10 | | | | 15 | 20 | 25 |
| GAG | CTC | CAC | GGC | TGG | CGC | 806 |
| Glu | Leu | His | Gly | Trp | Arg | |
| | | | 30 | | 35 | 40 |
| CTG | TGT | GCG | GCT | GAA | TCC | 854 |
| Leu | Cys | Ala | Ala | Glu | Ser | |
| | | 45 | | 50 | 55 | |
| CAG | TGC | CTG | GCA | GGC | CGG | 902 |
| Gln | Cys | Leu | Ala | Gly | Arg | |
| | | 60 | | 65 | 70 | |
| TGC | CAG | GCA | GCC | CTG | GAG | 950 |
| Cys | Gln | Ala | Ala | Leu | Glu | |
| | 75 | | | 80 | 85 | |
| CGC | TGC | AAG | CGG | GGC | ATG | 998 |
| Arg | Cys | Lys | Arg | Gly | Met | |
| 90 | | | | 95 | 100 | 105 |
| TGG | AGC | ATC | CAT | CTG | GGG | 1046 |
| Trp | Ser | Ile | His | Leu | Gly | |
| | | | 110 | | 115 | 120 |
| TCC | CCC | TAT | GAG | CCT | GTG | 1094 |
| Ser | Pro | Tyr | Glu | Pro | Val | |
| | | | 125 | | 130 | 135 |
| GCT | TCA | ATC | TTC | TCA | GGG | 1142 |
| Ala | Ser | Ile | Phe | Ser | Gly | |
| | | 140 | | | 145 | 150 |
| AGC | AAC | CAC | TGC | CTG | GAT | 1190 |
| Ser | Asn | His | Cys | Leu | Asp | |
| | 155 | | | | 160 | 165 |
| TGC | AAG | AAG | CTT | CGC | TCC | 1238 |
| Cys | Lys | Lys | Leu | Arg | Ser | |
| 170 | | | | 175 | 180 | 185 |
| TCT | CCC | ACC | GAA | CGC | TGC | 1286 |
| Ser | Pro | Thr | Glu | Arg | Cys | |
| | | | 190 | | 195 | 200 |
| CAG | TTC | TTT | GAC | CGT | GTG | 1334 |
| Gln | Phe | Phe | Asp | Arg | Val | |
| | | | 205 | | 210 | 215 |

1382
1430
1478
1526
1574
1622
1670
1718
1766
1814
1862
1910
1958
2006
2054
2103

CAGATATGAA CTCCCGCCTG ACAAATGGA AACACACGCA TACACACATG CCACACACAG 2163
 ACACACACAC AGACACACAC ACACACACAC ATACAGACGT CGACGCGGCC GC 2215

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Leu | Val | Phe | Pro | Ser | His | Tyr | Pro | Asp | Glu | Thr | Leu | Arg | Ser | Leu | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Ala | Ser | Pro | Ser | Ser | Leu | Gln | Gly | Ser | Glu | Leu | His | Gly | Trp | Arg | Pro | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Gln | Val | Asp | Cys | Val | Arg | Ala | Asn | Glu | Leu | Cys | Ala | Ala | Glu | Ser | Asn | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Cys | Ser | Ser | Arg | Tyr | Arg | Thr | Leu | Arg | Gln | Cys | Leu | Ala | Gly | Arg | Asp | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Arg | Asn | Thr | Met | Leu | Ala | Asn | Lys | Glu | Cys | Gln | Ala | Ala | Leu | Glu | Val | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Leu | Gln | Glu | Ser | Pro | Leu | Tyr | Asp | Cys | Arg | Cys | Lys | Arg | Gly | Met | Lys | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Lys | Glu | Leu | Gln | Cys | Leu | Gln | Ile | Tyr | Trp | Ser | Ile | His | Leu | Gly | Leu | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Thr | Glu | Gly | Glu | Glu | Phe | Tyr | Glu | Ala | Ser | Pro | Tyr | Glu | Pro | Val | Thr | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Ser | Arg | Leu | Ser | Asp | Ile | Phe | Arg | Leu | Ala | Ser | Ile | Phe | Ser | Gly | Thr | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Gly | Thr | Asp | Pro | Ala | Val | Ser | Thr | Lys | Ser | Asn | His | Cys | Leu | Asp | Ala | |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | | |
| Ala | Lys | Ala | Cys | Asn | Leu | Asn | Asp | Asn | Cys | Lys | Lys | Leu | Arg | Ser | Ser | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Tyr | Ile | Ser | Ile | Cys | Asn | Arg | Glu | Ile | Ser | Pro | Thr | Glu | Arg | Cys | Asn | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Arg | Arg | Lys | Cys | His | Lys | Ala | Leu | Arg | Gln | Phe | Phe | Asp | Arg | Val | Pro | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Ser | Glu | Tyr | Thr | Tyr | Arg | Met | Leu | Phe | Cys | Ser | Cys | Gln | Asp | Gln | Ala | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Cys | Ala | Glu | Arg | Arg | Arg | Gln | Thr | Ile | Leu | Pro | Ser | Cys | Ser | Tyr | Glu | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Asp | Lys | Glu | Lys | Pro | Asn | Cys | Leu | Asp | Leu | Arg | Ser | Leu | Cys | Arg | Thr | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |

Asp His Leu Cys Arg Ser Arg Leu Ala Asp Phe His Ala Asn Cys Arg
260 265 270

Ala Ser Tyr Arg Thr Ile Thr Ser Cys Pro Ala Asp Asn Tyr Gln Ala
275 280 285

Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe Asp Met Thr Pro Asn
290 295 300

Tyr Val Asp Ser Asn Pro Thr Gly Ile Val Val Ser Pro Trp Cys Asn
305 310 315 320

Cys Arg Gly Ser Gly Asn Met Glu Glu Glu Cys Glu Lys Phe Leu Arg
325 330 335

Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala Ile Gln Ala Phe Gly
340 345 350

Asn Gly Thr Asp Val Asn Met Ser Pro Lys Gly Pro Ser Leu Pro Ala
355 360 365

Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser Leu Pro Asp Asp Leu
370 375 380

Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile Thr Thr Cys Thr Ser
385 390 395 400

Ile Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser Lys Glu Leu Ser Met
405 410 415

Cys Phe Thr Glu Leu Thr Thr Asn Ile Ser Pro Gly Ser Lys Lys Val
420 425 430

Ile Lys Leu Asn Ser Gly Ser Ser Arg Ala Arg Leu Ser Ala Ala Leu
435 440 445

Thr Ala Leu Pro Leu Leu Met Leu Thr Leu Ala Leu
450 455 460

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1699 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 67..1257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

| | | | | | | |
|---|---|------------|------------|------------|------------|----|
| CGGGCCGCGT | CGACCGACGC | CCAGCACAGG | CAGAGCGCTG | CCGGGTCCGC | GGCGTCCAGA | 60 |
| CCCGCC | ATG GGG CTC TCC CGG AGC CCG CGA CCG CCG CCG CTA GTG ATC | 108 | | | | |
| Met Gly Leu Ser Arg Ser Pro Arg Pro Pro Pro Leu Val Ile | | | | | | |
| 1 | 5 | 10 | | | | |

| | | | | | | | | | | | | | | | | |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| CTG Leu 15 | CTA Leu | CTG Leu | GTG Val | CTG Leu | TCG Ser 20 | CTG Leu | TGG Trp | CTA Leu | CCC Pro | CTT Leu 25 | GGA Gly | ACA Thr | GGA Gly | AAC Asn | TCC Ser 30 | 156 |
| CTT Leu | CCC Pro | ACA Thr | GAG Glu | AAC Asn 35 | AGG Arg | CTT Leu | GTG Val | AAC Asn | AGC Ser 40 | TGT Cys | ACC Thr | CAG Gln | GCC Ala | AGA Arg 45 | AAA Lys | 204 |
| AAA Lys | TGC Cys | GAG Glu | GCT Ala 50 | AAT Asn | CCC Pro | GCT Ala | TGC Cys | AAG Lys 55 | GCT Ala | GCC Ala | TAC Tyr | CAG Gln | CAC His 60 | CTG Leu | GAC Asp | 252 |
| TCC Ser | TGC Cys | ACC Thr 65 | CCC Pro | AGT Ser | CTC Leu | AGC Ser | AGT Ser 70 | CCA Pro | CTG Leu | CCC Pro | TCA Ser | GGG Gly 75 | GAG Glu | TCT Ser | GCC Ala | 300 |
| ACA Thr 80 | TCT Ser | GCA Ala | GCG Ala | TGC Cys | CTT Leu | GAA Glu 85 | GCA Ala | GCA Ala | CAG Gln | CAA Gln | CTC Leu 90 | AGG Arg | AAC Asn | AGC Ser | TCT Ser | 348 |
| CTC Leu 95 | ATA Ile | GAC Asp | TGC Cys | AGG Arg | TGC Cys 100 | CAC His | CGG Arg | CGC Arg | ATG Met | AAG Lys 105 | CAC His | CAA Gln | GCT Ala | ACC Thr | TGT Cys 110 | 396 |
| CTG Leu | GAC Asp | ATT Ile | TAT Tyr | TGG Trp 115 | ACC Thr | GTT Val | CAC His | CCT Pro | GTC Val 120 | CGA Arg | AGC Ser | CTT Leu | GGT Gly | GAC Asp 125 | TAC Tyr | 444 |
| GAG Glu | TTG Leu | GAC Asp | GTC Val 130 | TCA Ser | CCC Pro | TAT Tyr | GAA Glu | GAC Asp 135 | ACA Thr | GTG Val | ACC Thr | AGC Ser | AAA Lys 140 | CCC Pro | TGG Trp | 492 |
| AAA Lys | ATG Met | AAT Asn 145 | CTC Leu | AGC Ser | AAG Lys | CTG Leu | AGC Ser 150 | ATG Met | CTC Leu | AAA Lys | CCA Pro | GAC Asp 155 | TCC Ser | GAC Asp | CTC Leu | 540 |
| TGC Cys 160 | CTC Leu | AAA Lys | TTT Phe | GCT Ala | ATG Met | CTG Leu 165 | TGT Cys | ACT Thr | CTT Leu | AAC Asn | GAC Asp 170 | AAG Lys | TGC Cys | GAC Asp | CGC Arg | 588 |
| CTC Leu 175 | CGA Arg | AAG Lys | GCC Ala | TAC Tyr | GGG Gly 180 | GAG Glu | GCG Ala | TGC Cys | TCA Ser | GGG Gly 185 | ATC Ile | CGC Arg | TGC Cys | CAG Gln | CGC Arg 190 | 636 |
| CAC His | CTC Leu | TGC Cys | CTA Leu | GCT Ala 195 | CAG Gln | CTG Leu | CGC Arg | TCC Ser | TTC Phe 200 | TTC Phe | GAG Glu | AAG Lys | GCG Ala | GCA Ala 205 | GAG Glu | 684 |
| TCC Ser | CAC His | GCT Ala | CAG Gln 210 | GGC Gly | CTG Leu | CTG Leu | CTG Leu | TGT Cys 215 | CCC Pro | TGT Cys | GCA Ala | CCC Pro | GAA Glu 220 | GAT Asp | GCG Ala | 732 |
| GGC Gly | TGT Cys | GGG Gly 225 | GAG Glu | CGC Arg | CGG Arg | CGC Arg | AAC Asn 230 | ACC Thr | ATC Ile | GCC Ala | CCC Pro | AGT Ser 235 | TGC Cys | GCC Ala | CTC Leu | 780 |
| CCG Pro | TCT Ser 240 | GTG Val | GCC Ala | CCC Pro | AAC Asn | TGC Cys 245 | CTA Leu | GAT Asp | CTT Leu | CGG Arg | AGC Ser 250 | TTC Phe | TGC Cys | CGT Arg | GCG Ala | 828 |
| GAC Asp 255 | CCT Pro | CTG Leu | TGC Cys | AGA Arg | TCA Ser 260 | CGC Arg | CTG Leu | ATG Met | GAC Asp | TTC Phe 265 | CAG Gln | ACC Thr | CAC His | TGC Cys | CAC His 270 | 876 |

(2) INFORMATION FOR SEQ ID NO:42:

(A) LENGTH: 397 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Gly Leu Ser Arg Ser Pro Arg Pro Pro Pro Leu Val Ile Leu Leu
1 5 10 15

Leu Val Leu Ser Leu Trp Leu Pro Leu Gly Thr Gly Asn Ser Leu Pro

| 20 | | | | | | | | | | 25 | | | | | 30 | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Thr | Glu | Asn | Arg | Leu | Val | Asn | Ser | Cys | Thr | Gln | Ala | Arg | Lys | Lys | Cys | | | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | | | |
| Glu | Ala | Asn | Pro | Ala | Cys | Lys | Ala | Ala | Tyr | Gln | His | Leu | Asp | Ser | Cys | | | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | | | |
| Thr | Pro | Ser | Leu | Ser | Ser | Pro | Leu | Pro | Ser | Gly | Glu | Ser | Ala | Thr | Ser | | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | | | |
| Ala | Ala | Cys | Leu | Glu | Ala | Ala | Gln | Gln | Leu | Arg | Asn | Ser | Ser | Leu | Ile | | | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | | | |
| Asp | Cys | Arg | Cys | His | Arg | Arg | Met | Lys | His | Gln | Ala | Thr | Cys | Leu | Asp | | | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | | | |
| Ile | Tyr | Trp | Thr | Val | His | Pro | Val | Arg | Ser | Leu | Gly | Asp | Tyr | Glu | Leu | | | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | | | |
| Asp | Val | Ser | Pro | Tyr | Glu | Asp | Thr | Val | Thr | Ser | Lys | Pro | Trp | Lys | Met | | | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | | | |
| Asn | Leu | Ser | Lys | Leu | Ser | Met | Leu | Lys | Pro | Asp | Ser | Asp | Leu | Cys | Leu | | | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | | | |
| Lys | Phe | Ala | Met | Leu | Cys | Thr | Leu | Asn | Asp | Lys | Cys | Asp | Arg | Leu | Arg | | | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | | | |
| Lys | Ala | Tyr | Gly | Glu | Ala | Cys | Ser | Gly | Ile | Arg | Cys | Gln | Arg | His | Leu | | | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | | | |
| Cys | Leu | Ala | Gln | Leu | Arg | Ser | Phe | Phe | Glu | Lys | Ala | Ala | Glu | Ser | His | | | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | | | |
| Ala | Gln | Gly | Leu | Leu | Leu | Cys | Pro | Cys | Ala | Pro | Glu | Asp | Ala | Gly | Cys | | | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | | | |
| Gly | Glu | Arg | Arg | Arg | Asn | Thr | Ile | Ala | Pro | Ser | Cys | Ala | Leu | Pro | Ser | | | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | | | |
| Val | Ala | Pro | Asn | Cys | Leu | Asp | Leu | Arg | Ser | Phe | Cys | Arg | Ala | Asp | Pro | | | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | | | |
| Leu | Cys | Arg | Ser | Arg | Leu | Met | Asp | Phe | Gln | Thr | His | Cys | His | Pro | Met | | | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | | | |
| Asp | Ile | Leu | Gly | Thr | Cys | Ala | Thr | Glu | Gln | Ser | Arg | Cys | Leu | Arg | Ala | | | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | | | |
| Tyr | Leu | Gly | Leu | Ile | Gly | Thr | Ala | Met | Thr | Pro | Asn | Phe | Ile | Ser | Lys | | | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | | | |
| Val | Asn | Thr | Thr | Val | Ala | Leu | Gly | Cys | Thr | Cys | Arg | Gly | Ser | Gly | Asn | | | | |
| 305 | | | | | 310 | | | | | | 315 | | | | 320 | | | | |
| Leu | Gln | Asp | Glu | Cys | Glu | Gln | Leu | Glu | Lys | Ser | Phe | Ser | Gln | Asn | Pro | | | | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | | | |
| Cys | Leu | Met | Glu | Ala | Ile | Ala | Ala | Lys | Met | Arg | Phe | His | Arg | Gln | Leu | | | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | | | | |
| Phe | Ser | Gln | Asp | Trp | Ala | Asp | Ser | Thr | Phe | Ser | Val | Met | Gln | Gln | Gln | | | | |
| | | 355 | | | | | 360 | | | | | 365 | | | | | | | |

157k
168

Asn Ser Ser Pro Ala Leu Arg Pro Gln Leu Arg Leu Pro Val Leu Ser
370 375 380

Phe Phe Ile Leu Thr Leu Ile Leu Leu Gln Thr Leu Trp
385 390 395

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Xaa | Xaa | Leu | Xaa | Xaa | Xaa | Pro | Xaa | Pro | Pro | Xaa | Xaa | Xaa | Met | 1 | 5 | 10 | 15 |
| Xaa | Leu | Xaa | Leu | Leu | Ser | Leu | Ala | Leu | Pro | Leu | Xaa | Xaa | Xaa | Leu | Gln | 20 | 25 | 30 | |
| Gly | Ala | Glu | Leu | Xaa | Gly | Xaa | Xaa | Arg | Leu | Xaa | Xaa | Asp | Cys | Val | Xaa | 35 | 40 | 45 | |
| Ala | Xaa | Xaa | Xaa | Cys | Xaa | Ala | Glu | Xaa | Xaa | Cys | Ser | Xaa | Xaa | Tyr | Arg | 50 | 55 | 60 | |
| Thr | Leu | Arg | Gln | Cys | Xaa | Ala | Gly | Xaa | Xaa | Xaa | Asn | Thr | Xaa | Leu | Ala | 65 | 70 | 75 | 80 |
| Ser | Gly | Xaa | Glu | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Cys | Xaa | Xaa | Ala | Xaa | Glu | 85 | 90 | 95 | |
| Xaa | Leu | Xaa | Xaa | Ser | Ser | Leu | Tyr | Asp | Cys | Arg | Cys | Lys | Arg | Gly | Met | 100 | 105 | 110 | |
| Lys | Lys | Glu | Xaa | Xaa | Cys | Leu | Xaa | Ile | Tyr | Trp | Ser | Xaa | His | Xaa | Xaa | 115 | 120 | 125 | |
| Leu | Xaa | Xaa | Gly | Asn | Xaa | Xaa | Leu | Glu | Xaa | Ser | Pro | Tyr | Glu | Pro | Xaa | 130 | 135 | 140 | |
| Val | Thr | Ser | Arg | Leu | Ser | Asp | Ile | Phe | Arg | Xaa | Xaa | Ser | Xaa | Xaa | Ser | 145 | 150 | 155 | 160 |
| Xaa | Xaa | Xaa | Xaa | Asp | Xaa | Xaa | Xaa | Xaa | Xaa | Lys | Ser | Asn | Xaa | Cys | Leu | 165 | 170 | 175 | |
| Asp | Ala | Ala | Lys | Ala | Cys | Asn | Leu | Asn | Asp | Xaa | Cys | Lys | Lys | Leu | Arg | 180 | 185 | 190 | |
| Ser | Ala | Tyr | Ile | Xaa | Xaa | Cys | Xaa | Xaa | Xaa | Xaa | Ser | Xaa | Xaa | Glu | Arg | 195 | 200 | 205 | |
| Cys | Asn | Arg | Arg | Lys | Cys | His | Lys | Ala | Leu | Arg | Gln | Phe | Phe | Asp | Lys | 210 | 215 | 220 | |

| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|-----|--|-----|--|--|--|--|-----|-----|
| Val | Pro | Xaa | Xaa | His | Xaa | Tyr | Gly | Met | Leu | Phe | Cys | Ser | Cys | Xaa | Xaa | 225 | | | 230 | | 235 | | | | | | 240 |
| Xaa | Asp | Xaa | Ala | Cys | Xaa | Glu | Arg | Arg | Arg | Gln | Thr | Ile | Xaa | Pro | Ser | | | | 245 | | 250 | | | | | 255 | |
| Cys | Ser | Tyr | Glu | Xaa | Xaa | Glu | Lys | Pro | Asn | Cys | Leu | Asp | Leu | Arg | Xaa | | | | 260 | | 265 | | | | | 270 | |
| Xaa | Cys | Arg | Thr | Asp | Xaa | Leu | Cys | Arg | Ser | Arg | Leu | Ala | Asp | Phe | Xaa | | | | 275 | | 280 | | | | | 285 | |
| Thr | Asn | Cys | Xaa | Xaa | Xaa | Xaa | Arg | Xaa | Val | Xaa | Ser | Cys | Xaa | Ala | Xaa | | | | 290 | | 295 | | | | | 300 | |
| Asn | Tyr | Xaa | Xaa | Cys | Leu | Xaa | Ala | Tyr | Xaa | Gly | Leu | Ile | Gly | Thr | Xaa | | | | 305 | | 310 | | | | | 315 | 320 |
| Met | Thr | Pro | Asn | Tyr | Val | Asp | Ser | Ser | Xaa | Thr | Xaa | Xaa | Xaa | Val | Ala | | | | 325 | | 330 | | | | | 335 | |
| Pro | Trp | Cys | Xaa | Cys | Arg | Gly | Ser | Gly | Asn | Xaa | Xaa | Glu | Glu | Cys | Glu | | | | 340 | | 345 | | | | | 350 | |
| Lys | Phe | Leu | Xaa | Phe | Phe | Xaa | Xaa | Asn | Pro | Cys | Leu | Xaa | Asn | Ala | Ile | | | | 355 | | 360 | | | | | 365 | |
| Gln | Ala | Phe | Gly | Asn | Gly | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | | | | 370 | | 375 | | | | | 380 | |
| Xaa | Pro | Xaa | Phe | Ser | Val | Xaa | Xaa | Xaa | Xaa | Xaa | Thr | Xaa | Thr | Xaa | Ala | | | | 385 | | 390 | | | | | 395 | 400 |
| Xaa | Arg | Val | Xaa | Xaa | Xaa | Pro | Ser | Leu | Xaa | Xaa | Xaa | Xaa | Ser | Xaa | Xaa | | | | 405 | | 410 | | | | | 415 | |
| Xaa | Xaa | Leu | Xaa | Thr | Xaa | Val | Xaa | Xaa | Xaa | Cys | Xaa | Xaa | Leu | Gln | Xaa | | | | 420 | | 425 | | | | | 430 | |
| Gln | Xaa | Leu | Lys | Xaa | Asn | Xaa | Ser | Xaa | Glu | Xaa | Xaa | Xaa | Cys | Phe | Xaa | | | | 435 | | 440 | | | | | 445 | |
| Glu | Leu | Thr | Thr | Asn | Xaa | Xaa | Xaa | Xaa | Ser | Gly | Xaa | Xaa | Xaa | Xaa | Ile | | | | 450 | | 455 | | | | | 460 | |
| Xaa | Xaa | Xaa | Ser | Xaa | Xaa | Ala | Xaa | Pro | Ser | Xaa | Ala | Leu | Xaa | Xaa | Leu | | | | 465 | | 470 | | | | | 475 | 480 |
| Pro | Val | Leu | Met | Leu | Thr | Ala | Leu | Ala | Xaa | Leu | Leu | Ser | Xaa | Xaa | Xaa | | | | 485 | | 490 | | | | | 495 | |
| Xaa | Ser | | | | | | | | | | | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 489 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Pro | Xaa | Xaa | Xaa | Xaa | Leu | Xaa |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Thr | Leu | Xaa | Ser | Leu | Xaa | Xaa | Pro | Leu | Xaa | Leu | Xaa | Xaa | Ser | Xaa | Xaa |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Xaa | Xaa | Xaa | Arg | Xaa | Xaa | Xaa | Asp | Cys | Val | Xaa | Ala | Xaa | Xaa | Xaa | Cys |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Xaa | Ala | Glu | Xaa | Xaa | Cys | Ser | Xaa | Xaa | Tyr | Arg | Thr | Leu | Arg | Gln | Cys |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Xaa | Ala | Gly | Xaa | Xaa | Xaa | Asn | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Ala |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Xaa | Xaa | Glu | Cys | Xaa | Xaa | Ala | Xaa | Glu | Xaa | Leu | Xaa | Xaa | Ser | Ser | Leu |
| | | | | 85 | | | | 90 | | | | | | 95 | |
| Tyr | Asp | Cys | Arg | Cys | Lys | Arg | Gly | Met | Lys | Lys | Glu | Xaa | Xaa | Cys | Leu |
| | | | 100 | | | | | 105 | | | | | | 110 | |
| Xaa | Ile | Tyr | Trp | Ser | Xaa | His | Xaa | Xaa | Leu | Xaa | Xaa | Gly | Xaa | Xaa | Xaa |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Leu | Glu | Xaa | Ser | Pro | Tyr | Glu | Xaa | Pro | Val | Thr | Ser | Arg | Leu | Ser | Asp |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ile | Phe | Arg | Xaa | Xaa | Ser | Xaa | Xaa | Ser | Xaa | Xaa | Xaa | Xaa | Asp | Xaa | Xaa |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Xaa | Xaa | Xaa | Lys | Ser | Asn | Xaa | Cys | Leu | Asp | Ala | Ala | Lys | Ala | Cys | Asn |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Leu | Asn | Asp | Xaa | Cys | Lys | Lys | Leu | Arg | Ser | Ala | Tyr | Ile | Xaa | Xaa | Cys |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Xaa | Xaa | Xaa | Xaa | Ser | Xaa | Xaa | Glu | Arg | Cys | Asn | Arg | Arg | Lys | Cys | His |
| | | | 195 | | | | 200 | | | | | 205 | | | |
| Lys | Ala | Leu | Arg | Gln | Phe | Phe | Asp | Lys | Val | Pro | Xaa | Xaa | His | Xaa | Tyr |
| | 210 | | | | 215 | | | | | | 220 | | | | |
| Gly | Met | Leu | Phe | Cys | Ser | Cys | Xaa | Xaa | Xaa | Asp | Xaa | Ala | Cys | Xaa | Glu |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Arg | Arg | Arg | Gln | Thr | Ile | Xaa | Pro | Ser | Cys | Ser | Tyr | Glu | Xaa | Xaa | Glu |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Xaa | Pro | Asn | Cys | Leu | Asp | Leu | Arg | Ser | Xaa | Cys | Arg | Thr | Asp | Xaa | Leu |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Cys | Arg | Ser | Arg | Leu | Ala | Asp | Phe | Xaa | Thr | Asn | Cys | Xaa | Pro | Xaa | Xaa |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Arg | Xaa | Xaa | Thr | Xaa | Cys | Xaa | Ala | Xaa | Asn | Tyr | Xaa | Xaa | Cys | Leu | Xaa |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Ala | Tyr | Xaa | Gly | Leu | Ile | Gly | Thr | Xaa | Met | Thr | Pro | Asn | Tyr | Val | Asp |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Xaa | Xaa | Thr | Xaa | Xaa | Xaa | Val | Ala | Pro | Trp | Cys | Xaa | Cys | Arg | Gly |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Ser | Gly | Asn | Xaa | Xaa | Glu | Glu | Cys | Glu | Lys | Phe | Leu | Xaa | Xaa | Phe | Xaa |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Xaa | Asn | Pro | Cys | Leu | Xaa | Asn | Ala | Ile | Gln | Ala | Phe | Gly | Asn | Gly | Xaa |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Asp | Val | Xaa | Met | Ser | Gln | Xaa | Xaa | Pro | Xaa | Xaa | Xaa | Xaa | Thr | Xaa | Ala |
| | 370 | | | | | 375 | | | | | | 380 | | | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Arg | Val | Xaa | Xaa | Xaa | Pro | Xaa | Leu | Xaa | Xaa |
| 385 | | | | | | 390 | | | | 395 | | | | | 400 |
| Xaa | Xaa | Ser | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Thr | Xaa | Val | Xaa | Xaa | Xaa | Cys |
| | | | 405 | | | | | | 410 | | | | | 415 | |
| Xaa | Xaa | Xaa | Gln | Xaa | Gln | Xaa | Leu | Lys | Xaa | Asn | Xaa | Ser | Xaa | Xaa | Xaa |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Xaa | Xaa | Cys | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Ser | Xaa | Xaa | Ala | Xaa | Xaa | Ser | Xaa |
| | | | 450 | | | | 455 | | | | 460 | | | | |
| Xaa | Leu | Xaa | Xaa | Leu | Pro | Val | Leu | Met | Leu | Thr | Xaa | Leu | Xaa | Xaa | Xaa |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| Leu | Xaa | Xaa | Xaa | Leu | Xaa | Glu | Thr | Ser | | | | | | | |
| | | | | 485 | | | | | | | | | | | |

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